

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2004, 02:34:49 ; Search time 4394 Seconds  
(without alignments)  
10623.679 Million cell updates/sec

Title: US-10-019-931-1  
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Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 5940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

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# ALIGNMENTS

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VERSION AX080458.1 GI:13159885  
KEYWORDS  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE

AUTHORS Varin, L. and Gidda, S.  
TITLE Methods, compositions and genetic sequences for modulating

flowering in plants, and plants genetically modified to flower  
early and tardily  
JOURNAL Patent: WO 0102589-A 1 11-JAN-2001;  
Varin, Luc (CA) ; Gidda, Satinder (CA)  
FEATURES Location/Qualifiers  
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## ORIGIN

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TITLE	REFERENCE	AUTHORS
Arabidopsis ORF clones	2 (bases 1 to 1080)	Kim, C.J., Chen, H., Cheuk, R., Shinn, P., Bowser, L., Carninci, P., Dale, J.M., Hwashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Kame, J., Kato, T., Kikuchi, S., Kikuchi, T., Kikuchi, Y., Kikuchi, Z., Kikuchi, A., Karlin-Neuman, G., Kawai, J., Lam, B., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Toriumi, M., Wong, C., Wu, H.C., Yamada, K., Yu, G., Shinozaki, K., Davis, R.W., Theologis, A., and Ecker, J.R.

**TITLE**  
JOURNAL  
Direct Submission  
Submitted (13-JUN-2003) Salk Institute Genomic Analysis Laboratory  
(SIGAL), Plant Biology Laboratory, The Salk Institute for  
Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,  
USA

COMMENT	USA
RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAPL cDNAs (RAPL cDNA : 'RIKEN Arabidopsis Full-Length cDNA') : Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Havareshizaki, Y. and Shinozaki, K.	

Hayasuzaki, T., and Shimotozaki, T.  
The Saik, Stanford, PGEC (SSP) Consortium members constructed and sequenced the PNI (OPF) clones using the RAPL cDNAs: Kim, C.J., Chang, H., Cheuk, R., Shinn, P., Bowser, L., Chan, M.M., King, C.M., Dai, J.-M., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Miranda, M., Nguyen, M., Oncidera, C.S., Palm, C.J., Quach, H.L., Souchnick, A., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yamada, K., Yu, C., Davis, R.W., Theologis, A., and Eckert, J.R.

Kim, C.J. (SSP/Salk) and Saki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs.

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Arabidopsis thaliana steroid sulfotransferase-like protein
(A55907010) mRNA, complete cds.
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VERSION AY099809.1 GI:20466685
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SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Euphorbia; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 1347)
Nguyen,M., Karlin-Neumann,G., Southwick,A., Lam,B., Miranda,M.,
Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,H.,
Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A.,
Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pham,P.K.,
Sakano,H., Sakurai,T., Satou,M., Seki,M., Shinn,P., Yamada,K.,
Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.
Direct Submission
Submitted (24-APR-2002) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
USA
e-mail for correspondence: arabsequence.stanford.edu

RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
Arabidopsis Full-length cDNA'): Seki,M., Narusaka,M., Ishida,J.,
Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the
sequencing and annotation of the RAFL cDNAs: Nguyen,M.,
Southwick,A., Karlin-Neumann,G., Lam,B., Miranda,M., Palm,C.J.,
Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K.,
Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shinn,P.,
Yamada,K., Ecker,J., Theologis,A. and Davis,R.W.

Nguyen,M. (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed
equally to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W.
(SSP/Stanford) contributed equally to this work as PIs.

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DEFINITION		AX080460		Version		AX080460.1		GI:13159886	
KEYWORDS		Arabidopsis thaliana (thale cress)		SOURCE		Arabidopsis thaliana		ORGANISM	
REFERENCE		Varin, L. and Gidda, S.		METHODS		Methods, compositions and genetic sequences for modulating		flowering in plants, and plants genetically modified to flower	
AUTHORS		Varin, Luc (CA) ; Gidda, Satinder (CA)		JOURNAL		Patent: WO 0102589-A 3 11-JAN-2001;		Varin, Luc (CA) ; Gidda, Satinder (CA)	
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ORGANISM	Arabidopsis thaliana		
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AUTHORS	Kim, C.J., Chen, H., Cheuk, R., Shinn, P., Bowser, L., Carninci, P., Chan, M.M., Chang, C.H., Dale, J.M., Hayashizaki, Y., Huan, V.W., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yamada, K., Yu, G., Yuan, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.		
TITLE	Arabidopsis ORF clones		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1044)		
AUTHORS	Kim, C.J., Chen, H., Cheuk, R., Shinn, P., Bowser, L., Carninci, P., Chan, M.M., Chang, C.H., Dale, J.M., Hayashizaki, Y., Huan, V.W., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yamada, K., Yu, G., Yuan, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.		

TITLE	JOURNAL		
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Direct Submission			
Submitted (17-APR-2003)			
Salk Institute Genomic Analysis Laboratory			
(StGnal), Plant Biology Laboratory, The Salk Institute for			
Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,			
USA			
RIKEN Genomic Sciences Center (GSC) members carried out the			
collection and clustering of RAFL cDNAs (RAFL CDNA: 'RIKEN			
Arabidopsis Full-Length cDNA') : Seki, M., Narusaka, M., Ishida, J.,			
Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,			
Hayashizaki, Y. and Shinozaki, K.			
The Salk, Stanford, PGSC (SSP) Consortium members constructed and			
sequenced the PUNI (ORF) clones using the RAFL cDNAs: Kim, C.J.,			
Chen, H., Cheuk, R., Shinn, P., Bowser, L., Chan, M.M., Chang, C.M.,			
Dale, J.M., Huan, V.W., Jones, T., Karlin-Neumann, G., Lam, B.,			
Lee, J.M., Lin, J., Miranda, M., Nguyen, M., Onodera, C.S., Palm, C.J.,			
Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C.,			
Yamada, K., Yu, G., Yuan, S., Davis, R.W., Theologis, A., and			
Ecker, J.R.			
Kim, C.J. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to			
this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk)			
contributed equally to this work as PIs.			



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Medicago truncatula clone mth2-22g8, WORKING DRAFT SEQUENCE, 3 ordered pieces.  
AC135566  
VERSION  
KEYWORDS  
SOURCE  
AC135566.13 GI:39752715  
HTG; HTGS\_PHASE2; HTGS\_DRAFT.  
Medicago truncatula (barrel medic)  
ORGANISM  
Medicago truncatula  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.  
1 (bases 1 to 111989)  
Shauli,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B., Cook,D., Kim,D. and Roe,B.A.  
Medicago truncatula BAC Clone mth2-22g8  
Unpublished  
REFERENCE  
2 (bases 1 to 111989)  
Shauli,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,

TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Cook,D., Kim,D. and Roe,B.A.  
Direct Submission  
Submitted (18-OCT-2002) Department Of Chemistry And Biochemistry,  
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,  
OK 73019, USA  
3 (bases 1 to 111989)  
Shauli,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,  
Cook,D., Kim,D. and Roe,B.A.  
Direct Submission  
Submitted (12-DEC-2003) Department Of Chemistry And Biochemistry,  
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,  
OK 73019, USA  
On Dec 12, 2003 this sequence version replaced gi:39573775.  
----- Genome Center  
Center: Department Of Chemistry And Biochemistry  
The University Of Oklahoma  
Center code:UOKNOR

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 3 contigs. Gaps between the contigs  
\* are represented as runs of N. The order of the pieces  
\* is believed to be correct as given, however the sizes  
\* of the gaps between them are based on estimates that have  
\* provided by the submittor.  
\* This sequence will be replaced  
\* By the finished sequence as soon as it is available and  
\* the accession number will be preserved.  
\* 1 11239: contig of 11239 bp in length  
\* 11240 11339: gap of unknown length  
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ORIGIN

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Matches 615; Conservative 0; Mismatches 346; Indels 9; Gaps 2;  
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Qy 466 CTCTCGGCTAGCAGCTCCCAAGAGCTTCGCAACCACTTACCGTTCCGTTCCCTAAAG 525  
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RESULT 12
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DEFINITION Medicago truncatula clone mth2-7k13, complete sequence.
ACCESSION AC144726
VERSION AC144726.6 GI:34365847
KEYWORDS HTG.
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE 1 (bases 1 to 138586)
Shauli,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.
Medicago truncatula BAC Clone mth2-7k13
Unpublished
JOURNAL
REFERENCE 2 (bases 1 to 138586)
Shauli,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.
Direct Submission
JOURNAL
TITLE Submitted (14-MAY-2003) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
REFERENCE 3 (bases 1 to 138586)
Shauli,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.
Direct Submission
JOURNAL
TITLE Submitted (15-JUL-2003) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
REFERENCE 4 (bases 1 to 138586)
Shauli,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.
Direct Submission
JOURNAL
TITLE Submitted (30-AUG-2003) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
COMMENT On Aug 30, 2003 this sequence version replaced gi:32567849.
----- Genome Center
Center: Department Of Chemistry
The University Of Oklahoma
Center code:UOKNOR
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Location/Qualifiers

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Best Local Similarity 55.5%; Pred. No. 1.4e-67;
Matches 540; Conservative 0; Mismatches 424; Indels 9; Gaps 2;

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LOCUS AC119410 linear HTG 18-DEC-2003
DEFINITION Medicago truncatula clone mth2-13n10, WORKING DRAFT SEQUENCE, 8
unordered pieces.
ACCESSION AC119410
VERSION AC119410.5 GI:40018695
KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT.
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE 1 (bases 1 to 107440)
AUTHORS Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.
TITLE Medicago truncatula BAC Clone mth2-13n10
JOURNAL Unpublished
AUTHORS
REFERENCE 2 (bases 1 to 107440)
AUTHORS Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.
TITLE Direct Submission
JOURNAL Submitted (26-APR-2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
REFERENCE 3 (bases 1 to 107440)
AUTHORS Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.
TITLE Direct Submission
JOURNAL Submitted (18-DEC-2003) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
COMMENT On Dec 18, 2003 this sequence version replaced gi:30231297.
----- Genome Center
Center: Department Of Chemistry And Biochemistry
The University Of Oklahoma
Center code:UOKNOR
* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 14717 22880: contig of 8164 bp in length
* 22881 22980: gap of unknown length
* 22981 38252: contig of 15272 bp in length
* 38253 38352: gap of unknown length
* 38353 54947: contig of 16495 bp in length
* 54948 54947: gap of unknown length
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* 66378 66477: gap of unknown length
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Best Local Similarity 56.0%; Pred. No. 2.1e-66;
Matches 548; Conservative 0; Mismatches 412; Indels 18; Gaps 3;

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FEATURES  
source

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RESULT 14
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LOCUS
DEFINITION
Medicago truncatula clone mth2-10a6, WORKING DRAFT SEQUENCE, 3
ordered pieces.
AC144476
VERSION
AC144476.6 GI:34576471
KEYWORDS
HTG; HTGS PHASE2; HTGS DRAFT.
SOURCE
Medicago truncatula
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE
1 (bases 1 to 119317)
Shauli,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.
Medicago truncatula BAC Clone mth2-10a6
Unpublished
2 (bases 1 to 119317)
Shauli,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.
Direct Submission
Submitted (22-APR-2003) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
3 (bases 1 to 119317)
Shauli,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.
Direct Submission
Submitted (12-SEP-2003) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
On Sep 11, 2003 this sequence version replaced gi:34365846.
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 101223: contig of 101223 bp in length
* 101224 101323: gap of unknown length
* 101324 108389: contig of 7066 bp in length
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FEATURES
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Query Match 23.5%; Score 252.8; DB 2; Length 119317;
Best Local Similarity 58.4%; Pred. No. 2,1e-66;
Matches 529; Conservative 0; Mismatches 352; Indels 25; Gaps 4;
QY 180 AACTCGTTACCTTACTATTCAGGGTTTGGTGCCCAAGCAAGAGANTCAAGCCAT 239

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RESULT 15
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LOCUS
DEFINITION
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unordered pieces.
AC147431
ACCESSION
AC147431.5 GI:39652661
VERSION
HTG; HTGS PHASE1; HTGS DRAFT.
KEYWORDS
Medicago truncatula (barrel medic)

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ORGANISM Medicago truncatula  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
Medicago.

REFERENCE 1 (bases 1 to 147510)  
AUTHORS Qin, B., Lin, S. and Roe, B.A.  
TITLE Medicago truncatula BAC Clone mth2-88g17  
JOURNAL Unpublished

REFERENCE 2 (bases 1 to 147510)  
AUTHORS Qin, B., Lin, S. and Roe, B.A.  
TITLE Direct Submission  
JOURNAL Submitted (18-NOV-2003) Department of Chemistry and Biochemistry,  
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,  
OK 73019, USA

REFERENCE 3 (bases 1 to 147510)  
AUTHORS Qin, B., Lin, S. and Roe, B.A.  
TITLE Direct Submission  
JOURNAL Submitted (12-DEC-2003) Department of Chemistry and Biochemistry,  
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,  
OK 73019, USA

COMMENT On Dec 10, 2003 this sequence version replaced gi:38708072.  
----- Genome Center  
Center: Department of Chemistry and Biochemistry  
The University of Oklahoma  
Center code: UOKNOR

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 6 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

\* 1 3309: contig of 3309 bp in length  
\* 3310 3409: gap of unknown length  
\* 3410 5938: contig of 2529 bp in length  
\* 5939 6038: gap of unknown length  
\* 6039 13001: contig of 6963 bp in length  
\* 13002 13101: gap of unknown length  
\* 13102 22529: contig of 9428 bp in length  
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\* 22630 69136: contig of 46507 bp in length  
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/clone="mth2-88g17"  
/clone\_lib="Medicago truncatula BAC"

ORIGIN  
Query Match 23.5%; Score 252.8; DB 2; Length 147510;  
Best Local Similarity 58.4%; Mismatch 352; Indels 25; Gaps 4;  
Matches 529; Conservative 0;

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QY 240 CATGCTTTCCAAACAGATTTCATCCCTC-GAAACGAGGTCGTTCTCGCCACCATAC 298  
DB 125207 AATCTCTTTCAAAATCATTTTCAAGCCAAAGATAGTAGTGTGTGTGCTCTATGC 125266

QY 299 CTAATCCGGTACACCTGGCTGCTAAAGCTTTTAACTTTTCAACATCCCTTAAACCGTCACCGGT 358  
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QY 359 TTGATCCGGTGTGCCTCGAGTACCAACACCTCTTTTCACTTCCACCTTCATGACCTTG 418

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QY 764 GGTACGAGGATCTCAAAGACGACATCGAGACCAACTTGAAGAGGCTTGCACACTTTCTTAG 823  
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QY 1064 CTTTCA 1069  
DB 126038 CATTTA 126043

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Job time : 4401 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2004, 02:28:29 ; Search time 491 Seconds  
(without alignments)  
9318.349 Million cell updates/sec

Title: US-10-019-931-1

Perfect score: 1077

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq\_29Jan04:\*

- 1: Geneseqn1980s:\*
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- 4: Geneseqn2001as:\*
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- 8: Geneseqn2003bs:\*
- 9: Geneseqn2003cs:\*
- 10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	1077	100.0	1077	4	Aaf29177 Hydroxyja
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4	843.6	78.3	1041	4	Aaf29178 Hydroxyja
5	229.2	21.3	980	7	Ada68055 Arabidops
6	229.2	21.3	981	6	Abz14244 Arabidops
7	229.2	21.3	981	7	Abz42036 Arabidops
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9	219.2	20.4	996	6	Abz13222 Arabidops
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14	184.2	17.1	271990	9	Add25213 Fertiliz
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16	172.8	16.0	1347	3	Aac37555 Arabidops
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20	153.8	14.3	1000	8	Adp23209 Envirome
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28	111.6	10.4	777	7	AAD54405	Aad54405 Lolium pe
29	108.6	10.1	1032	7	ADA71112	Ada71112 Rice gene
30	104	9.7	668	7	AAD54403	Aad54403 Lolium pe
31	100.8	9.4	1192	6	AAS20863	Aas20863 Z. marina
32	97	8.1	515	9	ABZ68951	Abz68951 Nucleotid
33	85.8	8.0	566	7	ABX56987	Abx56987 Arabidops
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## ALIGNMENTS

## RESULT 1

AAF29177  
ID AAF29177 standard; DNA; 1077 BP.

XX AAF29177;

XX 09-APR-2001 (first entry)

XX Hydroxyjasmonic acid sulfotransferase AtST2a gene.

KW Hydroxyjasmonic acid sulfotransferase; AtST2a; flowering time; cabbage;  
KW jasmonate; genetically modified plant; lettuce; sugar cane; carrot;  
KW increase vegetative growth; biomass increase; ds.

XX Arabidopsis thaliana.

XX WO200102589-A2.

XX 11-JAN-2001.

XX 06-JUL-2000; 2000WO-CA000801.

XX 06-JUL-1999; 99CA-02274873.

XX (VARI/) VARIN L.  
XX (GIDD/) GIDDA S.

XX Varin L, Gidda S;

XX WPI; 2001-159272/16.

XX P-PSDB; AAB49722.

XX Methods for modulating flowering in plants, particularly useful for  
XX plants used in the food-processing industry, involves modifying the  
XX endogenous level of compounds of the jasmonate family.

XX Claim 38; Fig 7; 50pp; English.

XX This invention relates to a method for modulating flowering in a plant.  
XX The method comprises modifying the endogenous level of at least one  
XX compound of the jasmonate family in a plant. The methods are used to  
XX produce plants which are genetically modified to flower early or tardily  
XX when compared to a corresponding plant that is not genetically modified,  
XX where the modified plant has an increased (flower early) or lowered  
XX (flower tardily) level of jasmonic acid, or a compound of the jasmonate  
XX family. The method is useful for modulating flowering, particularly for

CC plants that are used in the food-processing industry and plants with  
CC horticultural value. The method is particularly useful for e.g. delaying  
CC flowering time in crops like lettuce, cabbage, sugar cane or carrots,  
CC which results in increased vegetative growth and biomass. The present  
CC sequence represents the Arabidopsis thaliana At5g22a gene, which encodes  
CC an hydroxyjasmonic acid sulfotransferase protein, which can be used in  
CC the method of the invention  
XX

QY Sequence 1077 BP; 294 A; 257 C; 254 G; 272 T; 0 U; 0 Other;  
Query Match 100.0%; Score 1077; DB 4; Length 1077;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1077; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 121 GGGTAAAGTCCGAGTTCCGAAGAGATTCCTTCTTAAGGAGAGAGATCGAGA 180  
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QY 241 ATGCTTTTCAAAAACATTTTCCAAATCCCTCGAAAACGACGTCTTCGCCACCATACCT 300  
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DT 18-OCT-2000 (first entry)  
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XX  
KW Hybridisation assay; genetic mapping; gene expression control;  
XX protein identification; signal transduction pathway; metabolic pathway;  
XX promoter; termination sequence; ss.  
XX Arabidopsis thaliana.  
XX  
PN BP1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-00301439.  
XX  
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PR 01-APR-1999; 99US-0127462P.  
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PR 08-APR-1999; 99US-0128714P.  
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PR 28-APR-1999; 99US-0131449P.  
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PR 04-MAY-1999; 99US-0132484P.  
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Query Match 100.0%; Score 1077; DB 3; Length 1270;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1077; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 ATGGCTACCTCAAGCATGAAGAGATTCCTCAATGGGATCCCAAGTTTCTCCATGTCTAC 60
Db	64 ATGGCTACCTCAAGCATGAAGAGATTCCTCAATGGGATCCCAAGTTTCTCCATGTCTAC 123
Qy	61 AAGCTCGAGCTCTTAAGAGAGCAAACTCGGAGCTCCGAAAGCCGAAAGATGAA 120
Db	124 AAGCTCGAGCTCTTAAGAGAGCAAACTCGGAGCTCCGAAAGCCGAAAGATGAA 183
Qy	121 GGGCTAAGCTCGAGTTCGAAGAGATTTGGATTTCTTCTTAAGGAGAGATCGAGA 180
Db	184 GGGCTAAGCTCGAGTTCGAAGAGATTTGGATTTCTTCTTAAGGAGAGATCGAGA 243
Qy	181 ACTCGTTACCTTTACCTATTCCAAAGGTTTGGTCCCAAGCCAAAGAGATTCAGGCATC 240
Db	244 ACTCGTTACCTTTACCTATTCCAAAGGTTTGGTCCCAAGCCAAAGAGATTCAGGCATC 303
Qy	241 ATGCTTTTCCAAAAATTTCCAAATCCCTCGAAAAAGCAGCTGTTCTCGCCACCATACCT 300
Db	304 ATGCTTTTCCAAAAATTTCCAAATCCCTCGAAAAAGCAGCTGTTCTCGCCACCATACCT 363
Qy	301 AAATCCGGTACAACTCGGCTAAAGCTTTTAACTTTTACCATCTTAAACCGTCAACCGTTT 360
Db	364 AAATCCGGTACAACTCGGCTAAAGCTTTTAACTTTTACCATCTTAAACCGTCAACCGTTT 423
Qy	361 GATCCGGTTGCTCGAGTACCAACACCTCTTTTTCATCTTCCAAACCTCATGACCTTGTA 420
Db	424 GATCCGGTTGCTCGAGTACCAACACCTCTTTTTCATCTTCCAAACCTCATGACCTTGTA 483
Qy	421 CTTTCTTTCGAGTCAAGCTTTACGCCAAAGGAGATTTCCGATCTCTCGGTCTAGCC 480
Db	484 CTTTCTTTCGAGTCAAGCTTTACGCCAAAGGAGATTTCCGATCTCTCGGTCTAGCC 543
Qy	481 AGTCCAAAGAGCTTTCGCAACCTTACCGTTTCGGTTCCCTTAAAGGAAACGATCGAGAAA 540
Db	544 AGTCCAAAGAGCTTTCGCAACCTTACCGTTTCGGTTCCCTTAAAGGAAACGATCGAGAAA 603
Qy	541 CCCGGTGTGAAGGTCGTGTACTTGTGCGGGAACCCGTTTGACACATTCATCTCTTGTGG 600
Db	604 CCCGGTGTGAAGGTCGTGTACTTGTGCGGGAACCCGTTTGACACATTCATCTCTTGTGG 663
Qy	601 CATTCACCAACATCAATCCGAGTCAGTACCCAGCTCTTGTAGACCAAGCTTTT 660
Db	664 CATTCACCAACATCAATCCGAGTCAGTACCCAGCTCTTGTAGACCAAGCTTTT 723
Qy	661 GATCTGTATTCGGGGAGTGTATCGGGTTTGGCCCGTTTGGGAAACATGTTGGGATAC 720
Db	724 GATCTGTATTCGGGGAGTGTATCGGGTTTGGCCCGTTTGGGAAACATGTTGGGATAC 783
Qy	721 TGGAGAGAGCTTGAAGAGACCAAGAGAACTCTTTTAAAGTACGAGGATCTCAAA 780
Db	784 TGGAGAGAGCTTGAAGAGACCAAGAGAACTCTTTTAAAGTACGAGGATCTCAAA 843
Qy	781 GACGACATCGAGCAACCTTGAAGAGGCTTCCAACTTTCTTGAAGCTTCTTCCACCGAA 840
Db	844 GACGACATCGAGCAACCTTGAAGAGGCTTCCAACTTTCTTGAAGCTTCTTCCACCGAA 903
Qy	841 GAAAGAGCAAGAAAGGAGTGTGAAGGCTATCGCCGAGCTGTGTAGCTTCGAGAACTGTG 900
Db	904 GAAAGAGCAAGAAAGGAGTGTGAAGGCTATCGCCGAGCTGTGTAGCTTCGAGAACTGTG 963
Qy	901 AAGAAGTTGGAGGTGAAAGCTCAACCAAGTCGATCAAGACTTTGAGAACTCGATTCTTG 960
Db	964 AAGAAGTTGGAGGTGAAAGCTCAACCAAGTCGATCAAGACTTTGAGAACTCGATTCTTG 1023
Qy	961 TTTCCGAAGGAGAGAGTGAAGTGAATGGGTAACTATTGTACCTTCAAGTGGAAAGA 1020
Db	1024 TTTCCGAAGGAGAGAGTGAAGTGAATGGGTAACTATTGTACCTTCAAGTGGAAAGA 1083
Qy	1021 TTGTGAGCTTGTAGTGATGACAAAGTAGTGATCTGGTCTCACTTCAGGTTGAGC 1077
Db	1084 TTGTGAGCTTGTAGTGATGACAAAGTAGTGATCTGGTCTCACTTCAGGTTGAGC 1140

RESULT 3  
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AC AAC47848;  
XX  
DT 18-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 55342.  
XX  
KW Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway; metabolic pathway;  
KW promoter; termination sequence; ss.  
XX  
OS Arabidopsis thaliana.  
XX  
PN EP1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-00301439.  
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PR 05-MAR-1999; 99US-0123180P.  
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PR 25-MAR-1999; 99US-0126264P.  
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PR	16-AUG-1999;	99US-0149368P.			
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Query Match 99.7%; Score 1073.8; DB 3; Length 1273;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1075; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1	ATGGCTACCTCAAGCATGAAGAGCATTCCAATGGGATCCCAAGTTCTCCATGTGTAC	60
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QY	61	AAGCTCGAGCTCCTTAAAGAGGCAAACTCGCAGCTCCGAAAGCCGAAAGAGATGAA	120
DB	126	AGCTCGAGCTCCTTAAAGAGGCAAACTCGCAGCTCCGAAAGCCGAAAGAGATGAA	185
QY	121	GGCTAAGCTCGGATTCCAAGAGATGTGATTCCTCTTAAGGAGAGAGATGGAGA	180

Db 186 GGGCTAAGTCGAGTTTCCAGAGATGTTGGATTCTCTTCTTAAGGAGAGGATGGAGA 245  
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 Db 246 ACTCGTTACCTTTTACCTATTCCAGGGTGTGGCCAGCCAAAGAGATTCAAGCCATC 305  
 QY 241 ATGCTCTTTCAAAAACATTTCCAAATCCTCGAAGAACGACGTCTCTTCGCGCCACCATACCT 300  
 Db 306 ATGCTCTTTCAAAAACATTTCCAAATCCTCGAAGAACGACGTCTCTTCGCGCCACCATACCT 365  
 QY 301 AAATCCGGTACACCTGGCTTAAGCTTTTAACTTTACGATCTTAAACGTCACCGGTTT 360  
 Db 366 AAATCCGGTACACCTGGCTTAAGCTTTTAACTTTACGATCTTAAACGTCACCGGTTT 425  
 QY 361 GATCCGGTGTGCTCGAGTACCAACACCTCTTTTCACTTCCAAACCTCATGACCTTTGTA 420  
 Db 426 GATCCGGTGTGCTCGAGTACCAACACCTCTTTTCACTTCCAAACCTCATGACCTTTGTA 485  
 QY 421 CCTTTCTCGAGTACAAAGCTTTACGCAACGAGATGTTCCGATCTCTCGGTCGTAGCC 480  
 Db 486 CCTTTCTCGAGTACAAAGCTTTACGCAACGAGATGTTCCGATCTCTCGGTCGTAGCC 545  
 QY 481 AGTCCAGAGGTTCCGCAACCTTACCTCGTTCGTTCCCTAAAGGAAACGATCGAGAAA 540  
 Db 546 AGTCCAGAGGTTCCGCAACCTTACCTCGTTCGTTCCCTAAAGGAAACGATCGAGAAA 605  
 QY 541 CCCGGTGTGAAGTGTGTACTTGTGCGGGAACCCGTTTGACACATTCATCTCTTCGTGG 600  
 Db 606 CCCGGTGTGAAGTGTGTACTTGTGCGGGAACCCGTTTGACACATTCATCTCTTCGTGG 665  
 QY 601 CATTAACCAACACATCAAACTCGAGTCAAGTACGAGCCAGCTCTGTAGACCAAGCTTT 660  
 Db 666 CATTAACCAACACATCAAACTCGAGTCAAGTACGAGCCAGCTCTGTAGACCAAGCTTT 725  
 QY 661 GATCTGTTATTCGCGGAGTGTATCGGTTTGGCCGTTTGGCAACACATGTTGGGATAC 720  
 Db 726 GATCTGTTATTCGCGGAGTGTATCGGTTTGGCCGTTTGGCAACACATGTTGGGATAC 785  
 QY 721 TGGAGAGAGCTTTGAAGAGACCAAGAAAGTCTTTTAAAGGTACGAGGATCTCAAA 780  
 Db 786 TGGAGAGAGCTTTGAAGAGACCAAGAAAGTCTTTTAAAGGTACGAGGATCTCAAA 845  
 QY 781 GACCAATCGAGACCACTTGAAGAGCTTGCACATTTCTTAGAGCTTCCCTTTACCGAA 840  
 Db 846 GACCAATCGAGACCACTTGAAGAGCTTGCACATTTCTTAGAGCTTCCCTTTACCGAA 905  
 QY 841 GAAGAGGAACGAAAGGAGTTGTGAAGGCTATCGCGAGCTGTGTAGCTTCGAGATCTG 900  
 Db 906 GAAGAGGAACGAAAGGAGTTGTGAAGGCTATCGCGAGCTGTGTAGCTTCGAGATCTG 965  
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 QY 961 TTTCCGAAAGGAGAGTGAAGTGAAGTTGAGTTAACTATTGTCACTTCAAAAGTGAAGA 1020  
 Db 1026 TTTCCGAAAGGAGAGTGAAGTGAAGTTGAGTTAACTATTGTCACTTCAAAAGTGAAGA 1085  
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RESULT 4

AAF29178

ID AAF29178 standard; DNA; 1041 BP.

XX AAF29178;

AC AAF29178;

XX 09-APR-2001 (first entry)

DT Hydroxyjasmonic acid sulfoltransferase AtSt2b gene.

DE

XX

KW Hydroxyjasmonic acid sulfoltransferase; AtSt2b; flowering time; cabbage;  
 XW jasmonate; genetically modified plant; lettuce; sugar cane; carrot;  
 XX increase vegetative growth; biomass increase; ds.  
 OS Arabidopsis thaliana.

XX WO200102589-A2.

XX 11-JAN-2001.

XX 06-JUL-2000; 2000WO-CA000801.

XX 06-JUL-1999; 99CA-02274873.

XX (VARI/) VARIN L.

XX (GIDD/) GIDDA S.

XX Varin L, Gidda S;

XX WPI; 2001-159272/16.

XX P-PSDB; AAB49723.

XX Methods for modulating flowering in plants, particularly useful for

XX plants used in the food-processing industry, involves modifying the

XX endogenous level of compounds of the jasmonate family.

XX Claim 38; Fig 9; 50pp; English.

XX This invention relates to a method for modulating flowering in a plant.

XX The method comprises modifying the endogenous level of at least one

XX compound of the jasmonate family in a plant. The methods are used to

XX produce plants which are genetically modified to flower early or tardily

XX when compared to a corresponding plant that is not genetically modified,

XX where the modified plant has an increased (flower early) or lowered

XX (flower tardily) level of jasmonic acid, or a compound of the jasmonate

XX family. The method is useful for modulating flowering, particularly for

XX plants that are used in the food-processing industry and plants with

XX horticultural value. The method is particularly useful for e.g. delaying

XX flowering time in crops like lettuce, cabbage, sugar cane or carrots,

XX which results in increased vegetative growth and biomass. The present

XX sequence represents the Arabidopsis thaliana AtSt2b gene, which encodes

XX an hydroxyjasmonic acid sulfoltransferase protein, which can be used in

XX the method of the invention

XX Sequence 1041 BP; 287 A; 241 C; 242 G; 271 T; 0 U; 0 Other;

XX

SQ

Query Match 78.3%; Score 843.6; DB 4; Length 1041;

Best Local Similarity 89.8%; Pred. No. 1.8e-258;

Matches 945; Conservative 0; Mismatches 89; Indels 18; Gaps 3;

QY 31 ATGGCGATCCCAAGTTTCTCCATGTGTCAAGCTCCAGCTCCCTTAAAGAGGCAAACT 90

Db 1 ATGGCGATCCCAAGTTTCTCCATGTGTGTCAAGCCCGAGCTCCTTAAGGAGGCAAAAGC 60

QY 91 CGCGAGCTCCCGAAGCCGAAAGATGAAGGCTTAAGCTCGAGTTCGAAGATGTG 150

Db 61 G-----AAGGCCAAGAAAGAGAGGCTTAAGCTACGAGTTCGAAGATGTG 108

QY 151 GATTCCTCTTCTTAGGAGAGGATGGAGAACTCGTTACCTTTACCTTATTCAGAGGTTT 210

Db 109 GACTCTCTTCTTAGGAGAGAGGAGCGAGAAATGTTACCTTTACTTATTCAGAGGTTT 168

QY 211 TGGTGCCCAAGCCAAAGAGATTCAAGCCATCATGTCTTTTCCAAAACATTTCCAAATCCCTC 270

Db 169 CGGTGCCAAGCTAAGAGATTCAAGCTATACGCTTTTCCAAAACATTTTCAGTCCCTT 228

QY 271 GAAACGAGGCTGTCTCGCCACCATACCTAAATCCGCTACCACTCGCTAAAGCTTTA 330

Db 229 CCAGACGAGCTGTCTCGCCACCATACCTAAATCTGSCAACACCTGTTTAAAGCTTTA 288

QY 331 ACTTTTCAACCTCTTAAACCGTCAACCGGTTTTCATCCGGTTGCC---TCGAGTACCAACAC 387

Db 289 ACTTTTCAACCTCTTAAACCGTCAACCGGTTTTCATCCGGTTTTCATCCGGTTTTCATCCAGTTCGAGCAC 348





QY 772 GATCTCAAGACGACATCGAGCCAACTTGAAGAGGCTTGCACATTTCTTTAGAGCTTCT 831  
 DB 688 GAGCTTAAAGACGACGACGAGTTGAGATGAAGCGGATCGCGAGTTCTTTGGAAATGTGC 747  
 QY 832 TTCACCGAAGAGGAGGACGAAAGGAGTTGTGAAGCTATCCCGAGCTGTGTAGCTTC 891  
 DB 748 TTTATTGAAGAAGAGAA-----GTGAGAGAGATTGGAAGTTGTGTAGCTTT 795  
 QY 892 GAGAACTCTGAAGAGTTGGAGGTGAACAAGTCAACCAAGTCGATCAAGAACTTTGAGAAT 951  
 DB 796 GAGAGTTTAAAGTAATTTGGAAGTTTAAACAAGAGGGAATTTGCCAATGGAATAGAGACT 855  
 QY 952 CGATCTTGTTCGGAAGGAGGAGTGAAGTTGGGTTAACTATTGTTCACCTTCACAA 1011  
 DB 856 AAAAATTTCTTTAGAAAAGGAGGATTTGGAGATGGAGAGATACTTTGAGTGAGTCAATG 915  
 QY 1012 GTGGAAGATTGTGAGCCTTAGTGGATGACAAAGTTAGGTGATCTGGTCTCACTTT 1067  
 DB 916 GCAGAGGAAATTGATAGAACCAATTGAAGAGAGTTTAAAGGTTCTGGTCTTAAATT 971

RESULT 6

ABZ14244  
 ID ABZ14244 standard; DNA; 981 BP.

XX AC ABZ14244;

XX DT 21-JAN-2003 (first entry)

XX DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2049.

XX KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.

XX OS Arabidopsis thaliana.

XX PN WO200216655-A2.

XX PD 28-FEB-2002.

XX PF 24-AUG-2001; 2001WO-US026585.

XX PR 24-AUG-2000; 2000US-0227866P.

XX PR 26-JAN-2001; 2001US-0264647P.

XX PR 22-JUN-2001; 2001US-0300111P.

XX PA (SCRI) SCRIPPS RES INST.

XX PA (SYGN) SYNGENTA PARTICIPATIONS AG.

XX PI Harper JF, Kreps J, Wang X, Zhu T;

XX DR WPI; 2002-304127/34.

XX PT Identifying a stress condition to which a plant cell has been exposed and

XX PT producing plants with increased tolerance to these abiotic stresses.

XX PS Claim 144; SEQ ID NO 2049; 577pp + Sequence Listing; English.

The invention relates to identifying a stress condition to which a plant  
 cell has been exposed, comprising: (a) contacting nucleic acid  
 representative of expressed polynucleotides in the plant cell with an  
 array or probes representative of the plant cell genome; and (b)  
 detecting a profile of expressed polynucleotides in the plant cell  
 characteristic of a stress response. The method is useful in the  
 production of transgenic plants, cells and seeds and in producing plants  
 with increased tolerance to abiotic stress. The present sequence is that  
 of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used  
 in methods of the invention. Note: The sequence data for this patent is  
 not represented in the printed specification but is based on sequence  
 information supplied to Derwent by the European Patent Office

XX Sequence 981 BP; 283 A; 178 C; 228 G; 292 T; 0 U; 0 Other;

Query Match 21.3%; Score 229.2; DB 6; Length 981;  
 Best Local Similarity 54.9%; Pred. No. 3.8e-62;  
 Matches 525; Conservative 0; Mismatches 413; Indels 18; Gaps 3;  
 QY 112 GAAGATGAAGGGCTAAGCTGCGAGTTCCAAGAGATGTTGGAGTTCTTCTTAAAGAGAGA 171  
 DB 34 GAGATGAAGATCTGACACAGAAACAGAGCTCTGATCTCTCTCTTCTTAAAGAGAA 93  
 QY 172 GATGGAGAACTCGTTTACCTTACCTATTCGAAGGTTTGGTGCACCAAGCAAGAGATT 231  
 DB 94 GGTGGTTAGTGAGTGAATAATATGATTTCCAAGGACTTTGGCACACAAAGCTATTTTA 153  
 QY 232 CAAGCCATCATGCTCTTCCAAAAACATTTCCAATCCCTCGAAAAACGAGCTGTTCTCGCC 291  
 DB 154 CAAGAACTTGAATCTGCGCAAAACGCTTTGAAGCTAAAGATTCCGACATTTATCTCGTC 213  
 QY 292 ACCATACCTAAATCCGTTACAACTGGCTAAAGCTTTTAACTTTACCATCTTAAACGGT 351  
 DB 214 ACTAATCCTAAATCAGGTACCCTTGGTTAAAGCTCTTGTCTTCTCTCTTAAACCGA 273  
 QY 352 CACCGGTTGATCCGGTTGCGCTCGAGTACCAACCACTCTTTTCACTTCCAAACCTCAT 411  
 DB 274 CACAAGTT---TCCAGTTTCTTCTTCTGGTAACCATCTCTTCTGGTCACCAATCCACAC 330  
 QY 412 GACCTTGTACCTTTCTTCGAGTACAAGCTTTACGCAACGAGAGATGTTCCCGATCTCTCG 471  
 DB 331 CTTCTTGTGCGCTTCTTGAAGGAGTTTACTACGAGTCCCGAGATT---CGATTTCTCC 387  
 QY 472 GGTCTAGCCAGTCCGAAGACGTTGCCAACCCACTTACCGTTCCGTTCCCTTAAAGAAACG 531  
 DB 388 AGTTTGCCTTCTTCCAAGACTGATGAACACGACATATCGCATCTTTCGCTCCCGAGTCT 447  
 QY 532 ATCGAGAAACCGGTGTGAAGTCTGTGCTGTGCTGCGGAAACCGGTTTGACACATTCATC 591  
 DB 448 GTTAAGAGCTGTCTTGTGAAGTTGTGTATTTGTAGTAACCTTAAGGACATGTTGTG 507  
 QY 592 TCTTCGTGGCATTACCAACAACTCAATCCAGTCCAGTCAAGCCAGCTTCTCTAGAC 651  
 DB 508 TCTTTATGGCATTTTGGGAAAAAGCTAGCTCTCTGAGGAAACCGCGGATTTATCTTATCGAA 567  
 QY 652 CAAGCTTTTGTATCTGTTATGCGGGGAGTGTATGCGTTTGGCCGCTTTTGGGAAACATG 711  
 DB 568 AAAGCGTTGAAGCGTTTGTGAAGGAGTTTATAGTGAACCTTTTGGATCATATA 627  
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 QY 772 GATCTCAAGACGACATCGAGACCACTTGAAGAGGCTTGCACACTTCTTCTTAGAGCTTCT 831  
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 DB 748 TTTATTGAAGAAGAGAA-----GTGAGAGAGATTGTGAAGTTGTGTAGCTTT 795  
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 QY 1012 GTGGAAGATTGTCAAGCTTGTAGTGATGACAAGTTAGTGGATCTGTCTCATT 1067  
 DB 916 GCAGAGGAAATTGATAGAACCAATTGAAGAGAGTTTAAAGGTTCTGGTCTTAAATT 971

RESULT 7

ABZ42036  
 ID ABZ42036 standard; cDNA; 981 BP.

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Query Match      21.3%; Score 229.2; DB 3; Length 1043;
Best Local Similarity 54.9%; Pred. No. 4e-62;
Matches 525; Conservative 0; Mismatches 413; Indels 18; Gaps 3;

QY 112 GAAGATCAAGCGCTAAGCTCGAGTCCAGAGATGTTGAGTCTCTTCTCTTAAGGAGAGA 171
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QY 172 GGATGGAGAACTCGTTACCTTTTACTATTCCTCAAGGGTTTTGGTGCCCAAGCCAAAGATT 231
DB 156 GTTGGTTAGTGAGTGAATATATGAATTTCCAGGACTTTGGCACAACACAAGCTATTTTA 215
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DB 276 ACTAATCTTAATCAGTACCACTTGGTTAAAGCTCTTGTCTTGTCTCTCTTAACCGA 335
QY 352 CACCGGTTTGATCCGGTTGCTGAGTACCAACACACCTCTTTTCACTTCCAAACCTCAT 411
DB 336 CACAAGTT--TCCAGTTTCTTCTCTGTAACCATCTCTTCTGTGTCCACCAATCCACAC 392
QY 412 GACCTGTGACCTTCTTCGAGTACAACTTTACSCCAACGAGATGTTCCCGATCTCTCG 471
DB 393 CTTCTTGCCCTTCTTGGAAAGGATTTACTACGAGTCCCGAGATTT--CGATTTCTCC 449
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QY 532 ATCCAGAAACCCGGTGAAGTGTGTTGCTGTCGGAACCCGTTTGCACATTCATC 591
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QY 1012 GTGGAAGATTCTCAGCCTTAGTGGATGACAGTTAGGTGGATCTGGTCTCACTTT 1067
DB 978 GCAGAGAAATGTATAGAACCAATTGAAGAGAGTTTAAAGGTTCTGGTCTTAAT 1033

RESULT 9
ABZ13222
ID ABZ13222 standard; DNA; 996 BP.
XX ABZ13222;
AC ABZ13222;
XX 21-JAN-2003 (first entry)
DT 21-JAN-2003 (first entry)
XX Arabidopsis thaliana stress regulated gene SEQ ID NO 1027.
DE Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
XX Arabidopsis thaliana;
KW Arabidopsis thaliana.
XX Arabidopsis thaliana.
OS Arabidopsis thaliana.
XX Arabidopsis thaliana.
XX WO200216655-A2.
XX 28-FEB-2002.
PD 24-AUG-2001; 2001WO-US026685.
XX 24-AUG-2000; 2000US-0227866P.
PR 26-JAN-2001; 2001US-0264647P.
XX 22-JUN-2001; 2001US-0300111P.
XX (SCRI ) SCRIPPS RES INST.
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX Harper JF, Kreps J, Wang X, Zhu T;
XX WPI; 2002-304127/34.
XX
XX Identifying a stress condition to which a plant cell has been exposed and
XX producing plants with increased tolerance to these abiotic stresses.
XX Claim 144; SEQ ID NO 1027; 577pp + Sequence Listing; English.
XX
XX The invention relates to identifying a stress condition to which a plant
XX cell has been exposed, comprising: (a) contacting nucleic acid
XX representative of expressed polynucleotides in the plant cell with an
XX array or probes representative of the plant cell genome; and (b)
XX detecting a profile of expressed polynucleotides in the plant cell
XX characteristic of a stress response. The method is useful in the
XX production of transgenic plants, cells and seeds and in producing plants
XX with increased tolerance to abiotic stress. The present sequence is that
XX of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used
```

CC in methods of the invention. Note: The sequence data for this patent is  
CC not represented in the printed specification but is based on sequence  
CC information supplied to Derwent by the European Patent Office  
XX  
SQ Sequence 996 BP; 306 A; 199 C; 213 G; 278 T; 0 U; 0 Other;

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Query Match      20.4%; Score 219.2; DB 6; Length 996;
Best Local Similarity 53.0%; Pred. No. 6.1e-59;
Matches 520; Conservative 0; Mismatches 453; Indels 9; Gaps 2;

QY 86 AAACCTCGGAGCTCCGAAAGCCGAAAGAGATGAAGGCTAAGCTGGAGTTTCAAAGAGA 145
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DT 17-OCT-2000 (first entry)

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PR 29-SEP-1999; 99US-0156596P.
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PR 29-OCT-1999; 99US-0162142P.

Query Match 18.6%; Score 200.8; DB 3; Length 1212;
Best Local Similarity 53.0%; Pred. No. 5.1e-53;
Matches 514; Conservative 0; Mismatches 432; Indels 24; Gaps 3;

QY 104 AAGCGAAGAAGATCAAGGGCTAAGCTGCGAGTTCGAAGATGTCGAAGATGTCGATTCCTTCTTA 163
Db 71 AAGAGAAGAGAAGAAACCAAGTGAAGAAACCAAAAGTTGATCTCTTCACTTCCTT 130
QY 164 AGGAGAGAGATGGAGAAGTTCCTTACCTTTACCTTATTCGAAGGTTTGTGGTCCCAAGCCA 223
Db 131 CAGACATAGATTGCTCAGGGACCAAGTTGTACAAGTACCAAGGATGTTGGTACGACAAAG 190
QY 224 AAGAGATTCAAGCCATCATGCTTTCCAAACATTTCCATCCCTCGAAGAACGACGTCG 283
Db 191 ATATTCTCCAAGCAATCTCTCAATTTCAACAAAAAACTTTCAGCCCAAGAAACGGATATAA 250
QY 284 TTCTCGCCACCATTACCTAAATCCGGTACAACTCGGTAAAGCTTTAACTTTCAACCATCC 343
Db 251 TTGTTGCTTCTTTCCCAATCGGGTACGACTTGGCTCAAGGCACTACATTCGACTCG 310
QY 344 TTAACCGTCACGGTTTGATCCGTTGCTGAGTACCAACCAACCTCTCTTTTCACTTCCA 403
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419	ATTGTGACCAAGTTGCCATCATCTCCGAGATTGTTCTCAACCCACATGTCCTTTGATG	478	PR	08-APR-1999;	99US-0128714P
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518	CCTAAAGGAAACGATCGAGAAACCCGGTGTGAAGTGTGTTACTGTGTCGCGGAAACCCGT	577	PR	19-APR-1999;	99US-0130077P
			PR	21-APR-1999;	99US-0130498P
479	CGCTTAAAGTACCGTTCAAGAGTCTCCTTGCAGATCGTGTACGTGTGACGGAACGTCGA	538	PR	23-APR-1999;	99US-0130510P
			PR	23-APR-1999;	99US-0130891P
578	TTGACACATTCATCTCTTCGTGCGCATACACCAACCAACATCAAAATCCGAGTCACTGAGCC	637	PR	28-APR-1999;	99US-0131449P
			PR	30-APR-1999;	99US-0132048P
539	ATGACGTATTGATATCATCTTTGTGTTTGAAGATCTTCAATCCATGA-----GTGGAGAAACA	592	PR	30-APR-1999;	99US-0132407P
			PR	04-MAY-1999;	99US-0132484P
638	CAGTCTTTGTAGACCAAGCTTTTGTCTGTATTCGCCGGGAGTGATCGGGTTTGGCCCGT	697	PR	05-MAY-1999;	99US-0132485P
			PR	06-MAY-1999;	99US-0132486P
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698	TTTGGGAACACATGTTTGGGATCTCGAGAGAGAGCTTGAAGACACAGAGAAAGTCTTCT	757	PR	11-MAY-1999;	99US-0134256P
			PR	14-MAY-1999;	99US-0134218P
653	TATGGGAAAATGTGTTAGGCTATTTCGAGAGGAAGCTTGAAGATTCCTTAAGCATGTCCTTT	712	PR	14-MAY-1999;	99US-0134221P
			PR	14-MAY-1999;	99US-0134370P
758	TTTTTAAGGTACGAGGATCTCAAAGAAGCATCGAGACCAACTTTGAAGAGGCTTGCACACT	817	PR	18-MAY-1999;	99US-0134768P
			PR	19-MAY-1999;	99US-0134941P
713	TCATTGAGTACGAGGAGTTCAAGACGGAGCTCGTGTGCAAAATCAAGAGACTTTGCAGAGT	772	PR	20-MAY-1999;	99US-0135124P
			PR	21-MAY-1999;	99US-0135353P
818	TCATTGAGCTTCCTTTCAACCAAGAGAGAGAAAGGAGTTGTGAAGGCTATCGCG	877	PR	24-MAY-1999;	99US-0135629P
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773	TCATTGATTTCCATTCACAAAGAGAGAAAGATAGTGGAGGTGTAGACAAGATCTTGG	832	PR	27-MAY-1999;	99US-0136392P
			PR	28-MAY-1999;	99US-0136782P
878	AGCTGTCTAGCTTCGAGAACTCGAAGTTGAGAGTTGACAAAGTCAAAACAACTCGCATCA	937	PR	01-JUN-1999;	99US-0137222P
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938	AGAACTTTGAGAAATCGATTCTTGTTCGAAAGGAGAGTGAAGTGAAGTTTAACTATT	997	PR	08-JUN-1999;	99US-0138094P
			PR	10-JUN-1999;	99US-0138544P
893	AAGGAGTAAGTTTCAAGAGTTTTTTCCGTAAAGGGGAAGTTGGTGATTGGAAGAGTTATA	952	PR	10-JUN-1999;	99US-0138847P
			PR	14-JUN-1999;	99US-0139119P
998	TGTCACCTTCAAGTGGAAAGATTGTACGCCCTTAGTGGATGACAAAGTGAAGTGGATCTG	1057	PR	16-JUN-1999;	99US-0139452P
			PR	16-JUN-1999;	99US-0139453P
953	TGACTCTCTGAAATGGAACAAACAAATCGACATGATTGTTAGGAGAAACTTCAAGGCTCTG	1012	PR	17-JUN-1999;	99US-0139492P
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PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
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PR 23-SEP-1999; 99US-0155486P.
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PR 04-OCT-1999; 99US-0157117P.
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Query Match 18.0%; Score 194.2; DB 3; Length 1205;
Best Local Similarity 52.6%; Pred. No. 6.5e-51;
Matches 508; Conservative 0; Mismatches 433; Indels 24; Gaps 3;

QY 109 GAAGAAGATGAAGGCTAAGCTCGAGTTCGAAGAGATGTTGGATTCTCTTCTTAAGGAG 168
DB 64 GAAGAAGAGAAACCAAGTGAAGATTCGAAGATTTGATCTCTTCACTTCTTCAAC 123
QY 169 AGAGATGGAGAACTCGTTTACCTTATTCGAAGGGTTTGGTGCAAGCCAAAGAG 228
DB 124 ATAGATTGCTCTGGGACCAAGTTGTACAAAGTATCAAGGATGTGTGTACGATAAAGACATT 183
QY 229 ATTCAAGGCATCATGTCTTTCCAAACATTTCCATCCCTCGAAAGAGAGTGGTTCTC 288
DB 184 CTCGAAGCAATCTCAAAATCAACAAATCTTTGAGCCCAAGAAACCGATATAATGTT 243
QY 289 GCCACCATACCTAAATCCGGTACAACTGGGTGTAAGGCTTTAACTTTCAACATCCTTAAC 348
DB 244 GCTTCTTTCCCAAAATCAGGTACGACTTGGCTCAAGSCACTCACATTGCGACTCGCTCAA 303
QY 349 CGTACCCGGTTTGATCCGGTTGCCCTCGAGTACCAACCCCTCTTTTCACTTCCAAACCT 408
DB 304 AGATCAAAACATACCTTCAG-----AAAATCATCTCTGCTAACTCATATCTCT 351
QY 409 CATGACCTTTGTACCTTTCTTCGAGTACAAAGCTTTTACGCAACGAGAGATGTTCCCGATCTC 468
DB 352 CATGAGCTAGTCCGCTACTCGAGCTCGATCTTTATCTCAAAAGCTCGAAACCGGATATG 411
QY 469 TCGGGTCT-----AGCCAGTCCAAAGAGCTTCCGAAACCCACTTACCGTTGGTTCCTTA 522
DB 412 TCCAAGTTACCATCATCTCTCCGAGATGTTCTTCAACCCACATGTCTTTGATGGGCTT 471
QY 523 AAGGAACGATCGGAACACCGGTTGAGGTCGTGTACTTGTGCGCGAACCCGTTTTCAC 582
DB 472 AAGGTACCAATGAAGGAGACTCTTTGCAAGATGATGATGTGTGCAAGAACGTAAGAGAC 531
QY 583 ACATTCATCTCTCGTGGCATTACACCAACAACTCAATCCGAGTCAGTGCAGCCAGTC 642
DB 532 GTGTTGGTATCACTTTGGTGTTCGAAACCTCCATTAGTGAGAA-----ACAATTTA 585
QY 643 TTGCTAGACCAAGCTTTTGATCTGTATGCGGGGAGTGATCGGGTTGGCCCGTTTGG 702
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Db 1030 CAGGAATGGGACGGTGGCGGATTTGGCCAAACCACTGACCCAGAGATGGCCACAAGTT 1089  
Qy 1023 GTACAGCTTAGTGATGACAGAGTTAGTGGATCGTCTCACATT 1067  
Db 1090 GGATGGCATGTCAGGAGAGCTCAAAGGTTCTGGCCCTGCGCTT 1134

RESULT 14  
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ID ADD25213 standard; DNA; 271990 BP.  
XX AC ADD25213;  
XX AC 15-JAN-2004 (first entry)  
DT XX Fertility restorer protein genomic DNA sequence.  
DE XX fertility restorer protein; male sterile plant; viable pollen production;  
KW KW selection marker; ds; gene.  
XX OS Unidentified.  
XX PN WO2003006622-A2.  
XX XX 23-JAN-2003.  
XX PF 12-JUL-2002; 2002WO-US022217.  
XX PR 12-JUL-2001; 2001US-0305026P.  
XX PR 13-JUL-2001; 2001US-0305363P.  
XX PR 30-JUL-2001; 2001US-0308736P.  
XX XX (UYN-) UNIV MCGILL.  
PA (DNAL-) DNA LANDMARKS INC.  
XX XX Brown GG, Formanova N, Dendy C, Landry BS, Cheung W, Jin H;  
XX WPI; 2003-221734/21.  
XX XX New nuclear fertility restorer genes, useful for restoring fertility in  
PT cytoplasmic male-sterile plants such as Brassica napus plants, or for  
PT increasing production of viable pollen in a plant.  
XX Claim 1; SEQ ID NO 87; 191pp; English.  
XX PS The invention comprises the amino acid and coding sequences of isolated  
CC fertility restorer proteins. The DNA and protein sequences of isolated  
CC fertility restorer proteins. The DNA and protein sequences of the  
CC invention are useful for restoring fertility in male sterile plants, such  
CC as Brassica napus plants. The DNA and protein sequences of the invention  
CC are useful for increasing production of viable pollen in a plant. The DNA  
CC and protein sequences are also useful as selection markers to identify  
CC transformed plant cells. The present genomic DNA sequence contains coding  
CC sequences for fertility restorer proteins of the invention.  
XX SQ Sequence 271990 BP; 89597 A; 47325 C; 46930 G; 88078 T; 0 U; 60 Other;  
XX Query Match 17.1%; Score 184.2; DB 9; Length 271990;  
XX Best Local Similarity 53.5%; Pred. No. 1.8e-46;  
XX Matches 485; Conservative 0; Mismatches 403; Indels 19; Gaps 4;

Qy 114 AGATGAAGGCTAAGCTGCGAGTTCACAGAGATGTTGGATTCTCTCTTAAGGAGAGAGG 173  
Db 244850 AGACGACAAGATAAGTGAAGAAACCAAGGAGGTGATCTCTCGCTTCCTTCACACAGA 244791  
Qy 174 ATGGAGACTCGTTACTCTTACCTATTCAGAGGTTTGGTCCAGCCAGCCAAAGAGATTCA 233  
Db 244790 TTACCAAGGGCAATAGATTGTTAAATATCAAGGATGTTGGTATTATTAACACACCTCCA 244731  
Qy 234 AGCCATCATGCTTTTCCAAAACATTTCAATCCCTCGAAACGAGCTGTTCTCGCCAC 293  
Db 244730 AGGTGTC-TCAATTTCCAGAGAGTTTTCACCGGAGACATGATGTAATCATTTGCTTC 244672  
Qy 294 CATACTAAATCCGGTACACCTGGCTGCTAAAGCTTTAACTTTTCACTATCTTAAACCGTCA 353

Db 244671 GTACCCCAANTCAGGCACTACTTGGCTCAAGCCCTCACAGTCGTCTGCTTTGAGAGATC 244612  
Qy 354 CCGGTTTGATCCGGTTGCGTCGAGTACCAACACACCTCTTTTCACTTCCAAACCTTCATGA 413  
Db 244611 AAAGAACCACCTCTCTG-----ATCATCTCTCTATATCATATCTCTCATGG 244564  
Qy 414 CCTTGTAACCTTTCTTCGAGTACAAAGCTTTACGCCAACGGAGATGTTCCCGATCT---CTC 470  
Db 244563 CATTAACCATTTCTTGGAGATCGATGTGTACCAAGAAAGCTCAAGTCTCTTAAGCTAGCCAA 244504  
Qy 471 GGGTCTAGCCAGTCCAAGAAAGCTTCGCAACCCACCTTACCGTTTCGGTTCCCTAAAGGAAC 530  
Db 244503 GTTCTCAGCACCTCCGAGGCTGTTCTCGACTCACATGCCACTGCACACGATCCACGAAGC 244444  
Qy 531 GATCGAGAAACCGGTGTGAAGTCTGTACTTGTGCGGAAACCCGTTTGCACATTCAT 590  
Db 244443 ACTCAAGCACTCTCTCTGCAAGATTGTGTACGTGTGAGGAAACCGTGAAGGACACGTTGAT 244384  
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Qy 651 CCAAGCTTTTGATCTGTATTCGCGGGAGTGTATCGGGTTTGGCCGTTTGGGAACACAT 710  
Db 244323 GTCTATGTTTAAACGAGTCTCTCGATGGAACCAACTATTTTGGACCTTTTGGATCATCT 244264  
Qy 711 GTTGGGATCTGGAGAGAGCTTGAAGAGACCAAGAGAACTCTCTTTTAAAGGTAGA 770  
Db 244263 CTTGAGTTACTGGAGAGAAAGCTTGAAGAGACCAAGCATGTCTCTTTTCAAGGATAGA 244204  
Qy 771 GGATCTCAAAGACGACATCGAGACCAACTTGAAGAGGCTTGCACCTTTCTTAGAGCTTCC 830  
Db 244203 GGAGATGAAGCCGAGCTCTGTATCAGATCAAGAGACTTGGGACTTCTTGGGATGTC 244144  
Qy 831 TTTACCCAGAGAGGAAACGAAAGGAGTGTGTGAAGCTATCGCCGAGCTGTGTAGCTT 890  
Db 244143 TTTTACTAAGCAAGAAAGATAGTGGATCTGTGACCGGATCTTGGACCTCTGCTCTCT 244084  
Qy 891 CGAGAACTGAAGAAGTTGGAGGTGAACAAGTCAAAAGTCGATCAAGAACTTTTGAA 950  
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Qy 951 TCGATCTTGTTCGAAAGAGAGAGTGAAGTGAAGTGGTTAACTATTGTCACTTCA 1010  
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Db 243966 GGAGAAA 243960

RESULT 15  
ABZ68951

ID ABZ68951 standard; DNA; 1017 BP.

XX AC ABZ68951;

XX DT 28-MAY-2003 (first entry)

XX DE Nucleotide sequence of desulfoglucosinolate sulfotransferase AtST5a.

XX KW Plant; desulfoglucosinolate sulfotransferase; AtST5a; AtST5b; AtST5c;  
KW glucosinolate; transgenic plant; gene; ss.

XX OS Arabidopsis thaliana.

XX PH Key Location/Qualifiers

FT CDS 1..1017

FT /tag= a

FT /product= "desulfoglucosinolate sulfotransferase AtST5a"

XX PN WO2003010318-A2.



XX PD 06-FEB-2003.  
XX XX  
XX PF 24-JUL-2002; 2002WO-CA001144.  
XX XX  
XX PR 24-JUL-2001; 2001US-0307141P.  
XX XX  
XX PA (UYCO-) UNIV CONCORDIA.  
XX XX  
XX PI Varin L, Spertini D;  
XX XX  
XX DR WPI; 2003-248082/24.  
XX DR P-PSDB; ABP72962.  
XX XX  
PT Novel isolated or purified polypeptide having biological activity of  
PT desulfofoglucosinolate sulfotransferases, useful as enzymes involved in  
PT glucosinolate biosynthesis in transgenic plants.  
XX XX  
PS Claim 9; Page 54-55; 68pp; English.  
XX XX  
CC The present sequence encodes a plant desulfofoglucosinolate  
CC sulfotransferase, designated AtST5a. The specification also describe  
CC AtST5b and AtST5c. AtST5a and AtST5b are constitutively expressed in all  
CC parts of the plants, while AtST5c does not seem to be expressed in the  
CC early stage of development. These enzymes are involved in glucosinolate  
CC synthesis in plants. The desulfofoglucosinolate sulfotransferase  
CC polynucleotides are useful for modulating glucosinolate biosynthesis in  
CC transgenic plants  
XX XX  
SQ Sequence 1017 BP; 296 A; 205 C; 240 G; 276 T; 0 U; 0 Other;

Query Match 16.2%; Score 174.4; DB 7; Length 1017;  
Best Local Similarity 52.6%; Pred. No. 1.3e-44;  
Matches 494; Conservative 0; Mismatches 416; Indels 30; Gaps 4;

QY 134 AGTTCCAGAGATGTTGGATCTCTTCTTAAGGAGAGAGGATGGAACTCGTTA---CC 190  
DB 71 AGTATCAAGATTTTCATCGCTACACTTCCAAAGAGCAAGAGCTGGAGACCAAGATGATCT 130  
QY 191 TTTACCTATTCCAAAGGGTTTGGTGCCAAAGCAAGAGATTCAGCCATCATGCTCTTTCC 250  
DB 131 TAACCCATAGCTGGGACACTGGTGCGCAAGATGCTCTCGAAGGCTTTTTTCACGCTA 190  
QY 251 AAAAACAATTTCCAAATCCCTGAAACAGCGTGTCTTCGCCACCACTAAATCCGGTA 310  
DB 191 AAGACCATTTCCGAGCAGCAGCAACTGATTTCTCTGCTGTAGCTACCCCAAAACCCGGTA 250  
QY 311 CAACCTGGCTAAAGCTTTAACTTTTACCTTCCATCCCTTAACCGTTCACCGTTTGTATCCGGTTG 370  
DB 251 CAACCTGGCTCAAAGCACTAACTTACGCAATCGTCAATCGTTCTCGTTACGACGACG--- 307  
QY 371 CCTCGAGTACCACCAACCCCTCTTTTCACTTCCAAACCCCTCANGACCTTTGTACCTTTCTTCG 430  
DB 308 -----CGCAAAACCCACTCTCTCAAACGAAACCCCTCAGAGTTGTCTCTTACGTTG 358  
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DB 359 AGATCGACTTCGCGTTTACCCCAACCGTTGATGTTCTTCAAGACAGAAAGAACCC---AC 415  
QY 491 GGTTCGCAACCCACTTACCGTTTCGTTCCCTTAAAGGAAACGATCGAGAAACCCGGTGTGA 550  
DB 416 TTTTCTCTACTCATATCCCAACGGTTATTACCGGATTCGATGTCGAACTCTGGTTGTA 475  
QY 551 AGTTCGTGTACTGTGCGGAAACCGGTTTGACATTCATCTCTTCGTCGCATTACACCA 610  
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DB 536 ACAGGAGAGTCTCAAGAAAGTCAATTAGCGAGTCTTGAGACAGCTTTGATATGTTT 595  
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DB 596 GTAAAGGTTTATCTGTGTATGTCCTTATCTGGATCAATGTTTGGGTATTGGAAAGCTT 655  
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QY 911 AGGTGAACAAGTCAACAAGTCGATCAAGAA-----CTTTGAGAATCGATTCT 958  
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QY 959 TGTTTCGGAAGAGGAGAGTGTGATTTGGGTTAACTTATTTCTCACCCTTCACAGTGGAAA 1018  
DB 896 ATTTTAGGAAAGGAAAGGTTGGAGATTTGGGCTAATTTATTTGACTCTCTGAGATGCTGCTC 955  
QY 1019 GATTGTCAAGCTTGTAGTGGATGACAAAGTTAGGTGATCTGG 1058  
DB 956 GTATTGTGGCTTGTAGTGGAGGAGAAATTCAAAGATACCTGG 995

Search completed: August 17, 2004, 02:59:48  
Job time : 498 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 17, 2004, 02:43:04 ; Search time 3226 Seconds

(without alignments)  
9969.488 Million cell updates/sec

Title: US-10-019-931-1

Perfect score: 1077

Sequence: 1 atggctacctcaagcatgaa.....gttcactttcaggttgagc 1077

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: em\_gss\_hum:\*

18: em\_gss\_inv:\*

19: em\_gss\_pln:\*

20: em\_gss\_vrt:\*

21: em\_gss\_fun:\*

22: em\_gss\_man:\*

23: em\_gss\_mus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rod:\*

26: em\_gss\_pbg:\*

27: em\_gss\_vrl:\*

28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	541.4	50.3	811	28	BH733391
2	530	49.2	757	28	BZ062934
3	494.6	45.9	671	9	AU238005
4	486	45.1	574	9	AV827990

5	486	45.1	635	14	CB260303
6	484	44.9	523	9	AV442770
7	485	43.2	641	9	AV520946
8	462	42.9	585	14	CB260353
9	462	42.9	638	9	AV441110
10	453.6	42.1	727	14	CD837475
11	435.6	40.4	734	14	CD834047
12	421.4	39.1	531	9	AV442439
13	400.2	37.2	551	14	CD833738
14	367.2	34.1	657	14	CD822905
15	365.8	34.0	760	29	CC952179
16	365.6	33.9	566	14	H76376
17	363	33.7	379	14	CB257253
18	348	32.3	416	9	AV810198
19	346.2	32.1	643	9	AV441090
20	341.4	31.7	534	14	N65491
21	325	30.2	411	9	AV520947
22	317.8	29.5	479	14	T43254
23	305	28.3	341	9	AV442113
24	304.6	28.3	372	14	T13626
25	299.2	27.8	426	28	BH213349
26	296.8	27.6	373	14	T13706
27	277.8	25.8	419	9	AV800105
28	276.8	25.7	416	14	N37700
29	264.6	24.6	361	28	BH580029
30	263	24.4	698	13	BH831310
31	259.6	24.1	738	14	CF418052
32	257.2	23.9	795	14	CA799562
33	253	23.5	694	13	BH834467
34	249.6	23.2	781	14	CA782758
35	243.4	22.6	680	14	CB006702
36	238.8	22.2	329	14	T43998
37	238	22.1	739	28	BZ478554
38	237	22.0	475	14	T44617
39	230.2	21.4	353	14	T44081
40	228.8	21.2	406	9	AU229130
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43	221.2	20.5	934	29	CG919663
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45	219	20.3	402	28	BH756209

ALIGNMENTS

RESULT 1  
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LOCUS BH733391  
DEFINITION BOMIU60TR\_BO\_2\_3\_KB Brassica oleracea genomic clone BOMIU60,  
811 bp DNA linear GSS 20-FEB-2002  
ACCESSION BH733391  
VERSION BH733391  
KEYWORDS genomic survey sequence.  
SOURCE GSS.  
ORGANISM Brassica oleracea  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
REFERENCE 1 (bases 1 to 811)  
AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.  
TITLE Whole genome shotgun sequencing of Brassica oleracea  
JOURNAL Unpublished (2001)  
COMMENT Other\_GSSs: BOMIU60TF  
Contact: Chris Town  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA.  
Tel: 301-838-3523  
Fax: 301-838-0208  
Email: cdtown@tigr.org  
DNA is from a doubled haploid provided by Tom Osborn.  
Seq primer: TR  
Class: sheared ends.

FEATURES		Location/Qualifiers		SOURCE		ORGANISM	
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		/mol_type="genomic DNA"				Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	
		/strain="T01000H3"				rosids; eurosids II; Brassicales; Brassicaceae; Brassica.	
		/db_xref="taxon:3712"				1 (bases 1 to 757)	
		/clone="BOMTU60"				Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T.,	
		/clone_lib="BO_2.3 KB"				Nash, W., Rabinowicz, P.D. and Wilson, R.K.	
		/note="Vector: pHO51; Site 1: BstXI; 2-3 kb sheared				Whole genome shotgun reads from Brassica oleracea	
		genomic DNA inserted into pHO51 using BstXI linkers"				Unpublished (2002)	
						Contact: Richard K. Wilson	
						Genome Sequencing Center	
						Washington University School of Medicine	
						Email: submissions@watson.wustl.edu	
						Plate: llc02 row: b column: 11	
						Seq primer: -21UPpOT forward	
						Class: shotgun	
						High quality sequence start: 52	
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						/clone_lib="B.oleracea002"	
						/note="Vector: pOTW13; Whole genome shotgun library from	
						flowering buds. DNA was purified from a crude nuclear	
						prep using Brassica oleracea T01000H3 buds provided by	
						Thomas Osborn at the University of Wisconsin. Genomic	
						DNA was provided by Pablo Rabinowicz (CSHL) and the	
						shotgun library prepared at Washington University Genome	
						Sequencing Center."	
						source	

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650  ACCAAGCTTTTGTATCTGTATTGCGGGGAGTGATCGGGTTTGCCCGTTTGGGACACA 709
226  AAGAAGGTTTGTATCTGTATTGAGGGGAGTGATCGGGTTTCGGACCGTTTGGGACACA 167
710  TGTGGGATCTCGAGAGAGAGCTTGAAGAGACGAGAGAAAGTCTTCTTTTAAAGTAGC 769
166  TGCTGGGGTACTGGAGAGAGAGCTTGAAGAGACGAGAGAAAGTCTTCTTAAAGTAGC 107
770  AGATCTCAAGACGACATCGACACCACTTGAAGAGGCTTGCAACTTTCTTAGAGCTTC 829
106  AAGATCTGAAGAAGATATTGAGACTAACTTGAAGAAGCTTGCAAGTCTTCTTGGGGGTT 47
830  CTTTCA 835
46  CTTTCA 41

RESULT 3
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LOCUS AU238005 RAFL16 Arabidopsis thaliana cDNA clone RAFL16-75-F02 5',
DEFINITION mRNA sequence.
ACCESSION AU238005
VERSION AU238005.1 GI:19877174
SOURCE EST.
ORGANISM Arabidopsis thaliana (thale cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 671)
Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,
Akiyama, K., Enju, A., Oono, Y., Sakurai, T., Carninci, P., Kawai, J.,
Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shinagawa, A.,
Muranatsu, M., Hayashizaki, Y. and Shinozaki, K.
Large scale analysis of Arabidopsis full-length cDNA
Unpublished (2002)
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: msek@tc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et
al., submitted for publication) digested with BamHI and Sali. This
clone is in a modified pBluescript vector. Please visit our web
site (http://www.gsc.riken.go.jp/e/plant/index\_e.html) for further
details.
FEATURES             Location/Qualifiers
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                     /clone="RAFL16-75-F02"
                     /lab_host="DH10B"
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                     /note="Site_1: BamHI; Site_2: Sali; dark-grown"

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Matches 565; Conservative 0; Mismatches 59; Indels 15; Gaps 2;

10  TCAAGCATGAAGAGCATTCAATGGCGATCCCAAGTTCTCCATGTGTCCAAAGCTCGAG 69
45  TCAAGCATGAAGAGCATTCAATGGCGATCCCAAGTTCTCCATGTGTCCAAAGCTCGAG 104
70  CTCCTTAAAGAGCAAAATTCGCGAGTCCCGAGCGCAAGAGATGAAGGCTTAAGC 129

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105  CTCCTTAAAGAGGCAAAA-----GCGAAGCCCAAGAAAGAAAGGGCTAAGC 152
130  TCGAGATTCCAGAGAGATGTTGGATTCTCTTCTTAAGGAGAGAGATCGAGACTCGTTAC 189
153  TACGAGTTCCAGAGAGATGTTGGACTCTCTTCTTAAGGAGAGAGACGAGAAATCGTTAC 212
190  CTTTACCTATTCCAAAGGGTTTGGTGCCCAAGCAAGAGATTCAAGCCATCATGTCTTTTC 249
213  CTTTACTTATTCCAAAGGGTTTGGTGCCCAAGCAAGAGATTCAAGCTATCACGCTCTTTC 272
250  CAAAAACATTTCCAAATCCCTCGAAAAAGACGCTGTTCTGCGCACCATACCTAAATCCGGT 309
273  CAAAAACATTTTCAAGTCCCTTCCAGACGACGTTGTCTCGCCACCATACCTAAATCTGCG 332
310  ACAACCTGGCTAAAAGCTTTAACTTTTCAACCATCTTAAACCGTCAACCGGTTTGAATCCGGT 369
333  ACAACCTGGTTAAAGCTTTAACTTTTCAACCATCTTAAACCGTCAACCGGTTTGAATCCGGT 392
370  GCC---TCGAGTACCAACACCCCTCTTTTCACTTCCAAACCCCTCATGACCTGTGACTTTC 426
393  TCCTCATCAAGTTCGAGACCAACCCCTCTTCTCATATCCCAACCCCTCAGACCTGTACTTTC 452
427  TTCGAGTACAAGCTTTAGCCCAAGGAGATGTTCCCGATCTCTCGGCTAGCAGCTCA 486
453  TTCGAGTACAAGCTTTAGCCCAAGGAAATGTTCCCGATCTCTCGGCTAGCAGCTCA 512
487  AGAAGCTTCGCAACCCCACTTACCCTGTCGGTTCCCTTAAAGAAAGCATCGAGAAACCCGGT 546
513  AGAACATTTGCAACCCCACTACCGTTCGGTCCCTTAAAGATTTCGTCGAGAAATCCCACT 572
547  GTGAAGTTCGTTACTTGTGCGGAAACCGTTTGACACATTCATCTCTTCGTGGCAATAC 606
573  GTGAAGTTCGTTACTTGTGCGGAAACCGTTTGACACATTCATCTCTTCATGTGGCAATAC 632
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633  ATCACACATCACTTCCGAGTCAGTCAGCGAGCTCTTG 671

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DEFINITION mRNA sequence.
ACCESSION AV827990
VERSION AV827990.1 GI:19870050
SOURCE EST.
ORGANISM Arabidopsis thaliana (thale cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 574)
Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,
Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,
Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.
and Shinozaki, K.
Large scale analysis of Arabidopsis full-length cDNA (2002b)
Unpublished (2002)
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: msek@tc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et
al., submitted for publication) digested with BamHI and Sali. This
clone is in a modified pBluescript vector. Please visit our web
site (http://www.gsc.riken.go.jp/e/plant/index\_e.html) for further
details.
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ORIGIN
Query Match          45.9%; Score 494.6; DB 9; Length 671;
Best Local Similarity 88.4%; Pred. No. 1.9e-131;
Matches 565; Conservative 0; Mismatches 59; Indels 15; Gaps 2;

10  TCAAGCATGAAGAGCATTCAATGGCGATCCCAAGTTCTCCATGTGTCCAAAGCTCGAG 69
45  TCAAGCATGAAGAGCATTCAATGGCGATCCCAAGTTCTCCATGTGTCCAAAGCTCGAG 104
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## FEATURES

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## ORIGIN

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Best Local Similarity 99.2%; Pred. No. 5.2e-129;  
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QY 63 ATGCTACCTCAAGCATGAAGAGCATTCCTCAATGGCGATCCCAAGTTTCTCCATGTGTAC 122  
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QY 123 AAGCTCGAGTCTCTTAAGAAGGCAAACTCGCGAGTCCCGAAGCCGAAGAAGATGAA 182  
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QY 121 GGGCTAGTCGGAGTTCGAGAGATGTTGGATTCTCTCTAAGGAGAGAGATCGAGA 180  
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QY 483 CCTTTCTCGAGTACAAAGCTTTAGCCAAACGGAGATGTTCCCGATCTCTCGGGTCTAG 542  
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QY 543 CCAGTCCAAAGACGTTCCGCAACCCATTCACG 574  
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## RESULT 5

CE260303  
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DEFINITION 81-E9537-013-002-A22-T7R MP12-ADIS-013 Arabidopsis thaliana cDNA  
clone MP12p770A22Q 5-PRIME, mRNA sequence.

## ACCESSION

CE260303

## VERSION

CE260303.1 GI:32885076

## KEYWORDS

Est.  
Arabidopsis thaliana (thale cress)  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

## REFERENCE

1 (bases 1 to 635)  
Schmid, K.J., Soerensen, T.R., Stracke, R., Torjek, O., Altmann, T.,

## AUTHORS

Mitchell-Olds, T. and Weisshaar, B.

## TITLE

Large-scale identification and analysis of genome-wide

JOURNAL  
MEDLINE  
PUBMED  
COMMENT

single-nucleotide polymorphisms for mapping in Arabidopsis thaliana  
Genome Res. 13 (5), 1250-1257 (2003)  
22683290  
12799357  
Contact: Weisshaar, B  
ADIS DNA core facility at MP12  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@mpiz-koeln.mpg.de  
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Location/Qualifiers  
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/clone\_lib="MP12-ADIS-013"  
/note="Vector: pSPOR1; Site 1: SalI; Site 2: NotI; RNA from total, adult, 6 weeks old Arabidopsis thaliana (accession Nd-1) plants, grown in the greenhouse under long day conditions in soil treated for 24 hours with different stresses, (1) at 4 Grad C in the dark, (2) at 37 Grad C in the dark, (3) lying in the lab after removing from soil, (4) in the greenhouse after wounding with a forceps, (5) in the lab watering with a 150 mM NaCl solution, (6) at 26 Grad C in the light/UV; equal quantities of stressed plant material were pooled; library was made at the Max-Planck-Institute for Plant Breeding Research, Cologne, Germany; cloning sites SalI-NotI, primer sites and orientation:  
T7-SalI-CACGGTCCG-Sprime-cDNA-polyA-CC-NotI-SP6; Note: Sequencing granted in the context of the GABI Arabidopsis Verbund I: Genetic Diversity, 'Establishment of high-efficiency SNP-based mapping tools and development of methods for genome-wide mutation detection', PI: Bernd Weisshaar Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>. This clone is available from RZPD; contact RZPD (clone@rzpd.de) for further information."

## ORIGIN

Query Match 45.1%; Score 486; DB 14; Length 635;  
Best Local Similarity 98.0%; Pred. No. 5.5e-129;  
Matches 492; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
QY 576 GTTTGACACATTCTCTTCGTGGCATTACCAACAACATCAAAATCCGAGTCAGTGAG 635  
Db 1 GTTTGACACATTCTCTTCGTGGCATTACCAACAACATCAAAATCCGAGTCAGTGAG 60  
QY 636 CCCAGTCTGTAGACCAAGCTTTTGTCTCTATTGCGGGGAGTGATCGGTTTGCCCC 695  
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QY 696 GTTTTGGGAACACATGTTGGGATCTCTGGAGAGAGAGCTTGAAGAGACACAGAAAGTCTT 755  
Db 121 GTTTTGGGAACACATGTTGGGATCTCTGGAGAGAGAGCTTGAAGAGACACAGAAAGTCTT 180  
QY 756 CTTTAAAGGTACAGAGATCTCAAAGACGATCGAGACCAACTTGAAGGGCTTGCAC 815  
Db 181 CTTTAAAGGTACAGAGATCTCAAAGAGAGATCGAGACCAACTTGAAGGGCTTGCAC 240  
QY 816 TTTCTTAGGCTTCTTTTCCCGAAGAGAGAAACGAAAGGAGTTGTGAAGGCTATCGC 875  
Db 241 TTTCTTAGGCTTCTTTTCCCGAAGAGAGAAACGAAAGGAGTTGTGAAGGCTATCGC 300

Qy	876	CGAGCTGTGTAGCTTCGAGAAATCTGAAGAAGATTGGAGGTTGAAACAAGTCAACAAGTGCAT	935
Db	301	TGAGCTGTGTAGCTTCGAGAAATCTGAAGAAGATTGGAGTTGAAACAAGTCAACAAGTGCAT	360
Qy	936	CAAGAACTTTGAGAAATCGATTCTTTTCGGAAGAGGAAGTGTAGTGTGATTTGGGTTAACTA	995
Db	361	CAAGAACTTTGAGAAATCGATTCTTTTCGGAAGAGGAAGTGTAGTGTGATTTGGGTTAACTA	420
Qy	996	TTTGTCACCTTCACAAGTGGAAAGATTGTTCAGCCCTTAGTGGATGACAAAGTTAGTGGATC	1055
Db	421	TTTGTCACCTTCACAAGTGGAAAGATTGTTCAGCCCTTAGTGGATGACAAAGTTAGTGGATC	480
Qy	1056	TGGTCTCACCTTCAGGTTGAGC	1077
Db	481	TGGTCTCACCTTCAGGTTGAGC	502
RESULT 6			
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LOCUS	AV442770	523 bp	linear EST 14-NOV-2000
DEFINITION	AV442770 Arabidopsis thaliana above-ground organ two to six-week		
	old Arabidopsis thaliana cDNA clone AP228c04_r 5', mRNA sequence.		
ACCESSION	AV442770		
VERSION	AV442770.1	GI:7613187	
KEYWORDS	EST.		
SOURCE	Arabidopsis thaliana (thale cress)		
ORGANISM	Arabidopsis thaliana		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi		
REFERENCE	1 (bases 1 to 523)		
AUTHORS	Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.		
TITLE	A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries		
JOURNAL	DNA Res. 7 (3), 175-180 (2000)		
MEDLINE	20363093		
PUBMED	10907847		
COMMENT	Contact: Erika Asamizu The First Laboratory for Plant Gene Research Kazusa DNA Research Institute Yana 1532-3, Kisarazu, Chiba 292-0812, Japan Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/		
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Best Local Similarity	100.0%;	Pred. No. 1.9e-128;	
Matches 484;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
Qy	1	ATGGCTACCTCAAGCATGAAGAGATTCCAATGGCGATCCCAAGTTTCTCCATGTGTCCAC	60
Db	40	ATGGCTACCTCAAGCATGAAGAGATTCCAATGGCGATCCCAAGTTTCTCCATGTGTCCAC	99
Qy	61	AAGCTCGAGCTCCCTAAAGAAGGCCAAACTCGCGACGTCCCGAAAGCCGAAGAAGATGAA	120
Db	100	AAGCTCGAGCTCCCTAAAGAAGGCCAAACTCGCGACGTCCCGAAAGCCGAAGAAGATGAA	159
Qy	121	GGGCTAAGCTGCGAGTTCCAAGAGATTTGGATTCTCTTCTTAAGGAGAGAGATGGAGA	180
Db	160	GGGCTAAGCTGCGAGTTCCAAGAGATTTGGATTCTCTTCTTAAGGAGAGAGATGGAGA	219

Db 641 AACATCAATCCGAGTCAGTGAGCCAGCTTGTCTAGACCAAGCTTTTGATCTGTATTGC 582

Qy 673 CGGGAGTGATCGGTTTGGCCGTTTGGGAACAACATGTTGGGATCTGGAGAGAGGC 732

Db 581 CGGGAGTGATCGGTTTGGCCGTTTGGGAACAACATGTTGGGATCTGGAGAGAGGC 522

Qy 733 TTGAAGAGACAGAGAAGCTCTCTTTTAAAGTACGAGGATCTCAAGAGCATCTCGAG 792

Db 521 TTGAAGAGACAGAGAAGCTCTCTTTTAAAGTACGAGGATCTCAAGAGCATCTCGAG 462

Qy 793 ACCAATTTGAAGAGCTTGAACATTTCTTAGAGCTTCTTTTCCACGAGAGGAAACGA 852

Db 461 ACCAATTTGAAGAGCTTGAACATTTCTTAGAGCTTCTTTTCCACGAGAGGAAACGA 402

Qy 853 AAGGGAGTTGAAGGCTATCGCGAGCTGTAGCTTCAGAGATCTGAGAGTTGGAG 912

Db 401 AAGGGAGTTGAAGGCTATCGCGAGCTGTAGCTTCAGAGATCTGAGAGTTGGAG 342

Qy 913 GTGAACAAGTCAACAAGTCGATCAAGAACTTTGAGAACTCTTGTGTTTCGGAAGGA 972

Db 341 GTGAACAAGTCAACAAGTCGATCAAGAACTTTGAGAACTCTTGTGTTTCGGAAGGA 282

Qy 973 GAAGTGAAGTGGGTTAACTATTGTCTACCTTCAAGTGAAGATTTGAGCCTTA 1032

Db 281 GAAGTGAAGTGGGTTAACTATTGTCTACCTTCAAGTGAAGATTTGAGCCTTA 222

Qy 1033 GTGATGACAGTTAGTGGATCTGCTCTCACTTTACAGTTGAGC 1077

Db 221 GTGATGACAGTTAGTGGATCTGCTCTCACTTTACAGTTGAGC 177

RESULT 8  
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LOCUS 77-E011179-013-009-J20-TJR MP12-ADIS-013 Arabidopsis thaliana cDNA  
DEFINITION clone MP12p770J0209 5-PRIME, mRNA sequence.

ACCESSION CB260353.1 GI:32885126  
VERSION CB260353.1  
KEYWORDS EST.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Brassicales; Brassicaceae; Arabidopsi.  
1 (bases 1 to 585)  
Schmid,K.J., Soerensen,T.R., Stracke,R., Torjek,O., Altmann,T.,  
Mitchell-Olds,T. and Weissshaar,B.  
Large-scale identification and analysis of genome-wide  
single-nucleotide polymorphisms for mapping in Arabidopsis thaliana  
Genome Res. 13 (6), 1250-1257 (2003)

Genome Res. 13 (6), 1250-1257 (2003)  
22683290  
12799357  
Contact: Weissshaar B  
ADIS DNA core facility at MP12  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weissshaar@mpiz-koeln.mpg.de  
Insert Length: 585 Std Error: 0.00  
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Location/Qualifiers

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/note="vector: pSPORT1; site 1: SalI; site 2: NotI; RNA from total, adult, 6 weeks old Arabidopsis thaliana (accession Nd-1) plants, grown in the greenhouse under long day conditions in soil treated for 24 hours with different stresses, (1) at 4 Grad C in the dark, (2), at 37 Grad C in the dark, (3) lying in the lab after removing from soil, (4) in the greenhouse after wounding with a forecups, (5) in the lab watering with a 150 mM NaCl solution, (6) at 26 Grad C in the light/UV; equal quantities of stressed plant material were pooled; library was made at the Max-Planck-Institute for Plant Breeding Research, Cologne, Germany; cloning sites SalI-NotI, primer sites and orientation:  
T7-SalI-CCACGGCTCG-Sp1-CDNA-polyA-CC-NotI-SP6; Note: Sequencing granted in the context of the GABI Arabidopsis Verbund I: Genetic Diversity, 'Establishment of high-efficiency SNP-based mapping tools and development of methods for genome-wide mutation detection', PI: Bernd Weissshaar Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>. This clone is available from RZPD; contact rzpd (clone@rzpd.de) for further information."

## ORIGIN

Query Match 42.9%; Score 462; DB 14; Length 585;  
Best Local Similarity 100.0%; Pred. No. 4,6e-122;  
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 616 ATCAATCCGAGTCAGTGAGCCAGCTTTGCTAGACCAAGCTTTTGATCTGTATTGCGG 675

Db 1 ATCAATCCGAGTCAGTGAGCCAGCTTTGCTAGACCAAGCTTTTGATCTGTATTGCGG 60

Qy 676 GAGTGATCGGTTTGGCCGTTTGGGAACAACATGTTGGGATCTGGAGAGAGCTTG 735

Db 61 GAGTGATCGGTTTGGCCGTTTGGGAACAACATGTTGGGATCTGGAGAGAGCTTG 120

Qy 736 AAGACACAGAGAAGCTCTCTTTTAAAGTACGAGGATCTCAAGAGCATCGAGACC 795

Db 121 AAGACACAGAGAAGCTCTCTTTTAAAGTACGAGGATCTCAAGAGCATCGAGACC 180

Qy 796 AACTTGAAGAGCTTGCACACTTCTTAGAGCTTCTTACCGAAGAGGAAACGAAAG 855

Db 181 AACTTGAAGAGCTTGCACACTTCTTAGAGCTTCTTACCGAAGAGGAAACGAAAG 240

Qy 856 GAGTTGTAAGGCTATCGCGAGCTGTAGCTTCGAGATCTCAAGAGTTGAGGTG 915

Db 241 GAGTTGTAAGGCTATCGCGAGCTGTAGCTTCGAGATCTCAAGAGTTGAGGTG 300

Qy 916 AACAAAGTCAACAAGTCGATCAAGAACTTTGAGAACTCGATTCTTGTTCGAAAGGAGAA 975

Db 301 AACAAAGTCAACAAGTCGATCAAGAACTTTGAGAACTCGATTCTTGTTCGAAAGGAGAA 360

Qy 976 GTGAGTGAATGGTTAACTATTGTCTACCTTCAAGTGAAGATTTGAGCCTTAGTG 1035

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Qy 1036 GATGACAAAGTTAGTGGATCTGCTCACTTTCAGTTGAGC 1077

Db 421 GATGACAAAGTTAGTGGATCTGCTCACTTTCAGTTGAGC 462

## RESULT 9

AV441110/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AV441110 638 bp mRNA linear EST 14-NOV-2000  
AV441110 Arabidopsis thaliana above-ground organ two to six-week  
Old Arabidopsis thaliana cDNA clone AP228c04\_f 3', mRNA sequence.  
AV441110  
AV441110.1 GI:7611490  
EST.  
Arabidopsis thaliana (thale cress)  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;



rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 1 (bases 1 to 638)  
 Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.  
 A large scale analysis of cDNA in Arabidopsis thaliana: Generation  
 of 12,028 non-redundant expressed sequence tags from normalized and  
 size-selected cDNA libraries  
 DNA Res. 7 (3), 175-180 (2000)  
 MEDLINE 20363093  
 PUBMED 10907847  
 COMMENT  
 Contact: Erika Asamizu  
 The First Laboratory for Plant Gene Research  
 Kazusa DNA Research Institute  
 Yana 1532-3, Kisarazu, Chiba 292-0812, Japan  
 Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.  
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 Qy 856 GGAGTTGTGAAGGCTATCGCGAGCTGTAGCTTCGAGAAATCTGAAGAAGTTGGAGGTG 915  
 Db 398 GGAGTTGTGAAGGCTATCGCGAGCTGTAGCTTCGAGAAATCTGAAGAAGTTGGAGGTG 339  
 Qy 916 AACAGTCAACAGTCGATCAAGAACTTTGAGAAATCGATCTGTTCGGAAGAGGAA 975  
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 Qy 976 GTGAGTGATGGGTAACTAATTGTCACTTCAAGTGAAGAAGTTGTCAAGCTTAGTG 1035  
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 Qy 1036 GATGACAAAGTGTGATCTGGTCTCACTTTCAGGTTGAGC 1077  
 Db 218 GATGACAAAGTGTGATCTGGTCTCACTTTCAGGTTGAGC 177  
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 DEFINITION BN45.052G01F020104 BN45 Brassica napus cDNA clone BN45052G01, mRNA  
 sequence.  
 CD837475  
 ACCESSION  
 CD837475.1 GI:32519415

EST.  
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 Brassica napus  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
 1 (bases 1 to 727)  
 Genoplatane.  
 Genoplatane, a major partnership french program in plant genomics  
 Unpublished (2003)  
 Contact: Genoplatane  
 Genoplatane  
 93, rue Henri Rochefort 91025 EVRY CEDEX France  
 Tel: 33 1 69 47 54 00  
 Fax: 33 1 69 47 54 10  
 This sequence has been generated in the framework of the french  
 plant genomics programme 'Genoplatane' (http://www.genoplatane.com  
 and http://genoplatane-info.inbio.gen.fr).  
 Location/Qualifiers  
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 /db\_xref="taxon:3708"  
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 Qy 1 ATGGCTACCTCAAGCATGAGAGCATTC--AAATGGCGATCCCAAGTTTCTCCATGTGT 57  
 Db 51 ATGGCGACCTCAAGCATCAAGAGTGTTCATTAATGGCGATCCCAAGTTTCTCCATTTGC 110  
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 Qy 412 GACCTTGATCTTCTTCGAGTACAAGCTTTACGCAACGAGAGATGTTCCCATCTCTCG 471  
 Db 462 GACCTCGTACCTTCTTGGAGTACAAGCTTTACGCAACGAGAGATGTTCCCATCTCTCG 521  
 Qy 472 GGTCTAGCCAGTCCAGAACGTTTCGCAACCCACTTACCGTTTCGGTTTCCCTTAAGGAAAG 531  
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 Qy 532 ATCGAGAAACCCGGTGTGAAGTCTGTGACTTGTCCCGGAAACCCGTTTGACATTCATC 591  
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QY 285 TCTCGCCACCATCACTTAATCCGGTACAACTCGCTAAAAGCTTTAACTTACCATCT 344  
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QY 642 CTTGCTAGACCAAGCTTTTGCATCTGTATTCGCGGGAGT 680  
Db 481 CTTGCTAGACCAAGCTTTTGCATCTGTATTCGCGGGAGT 519

RESULT 13  
CD833738  
LOCUS  
DEFINITION  
CD833738 651 bp mRNA linear EST 10-JUL-2003  
sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Brassica napus (rape)  
Brassica napus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Genoplante.  
Genoplante, a major partnership french program in plant genomics  
Unpublished (2003)  
Contact: Genoplante  
Genoplante  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplante' (<http://www.genoplante.com>  
and <http://genoplante-info.infobiogen.fr>).

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Matches 501; Conservative 0; Mismatches 88; Indels 18; Gaps 3;

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Db 525 GGTCTAGTGTAGTCCAAAGAACATTCGCAACACGTCCTTTTCGGTTCTCTCAAGGGCTCC 584  
QY 532 ATCGAGAAACCGGTTGTAAGGTCGTGTACTTGTCCGGAACCCCTTTTGAACATTCATC 591  
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QY 592 TCTTCGT 598  
Db 645 TCTTCGT 651

RESULT 14  
CD822905  
LOCUS  
DEFINITION  
CD822905 657 bp mRNA linear EST 10-JUL-2003  
sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Brassica napus (rape)  
Brassica napus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Genoplante.  
Genoplante, a major partnership french program in plant genomics  
Unpublished (2003)  
Contact: Genoplante  
Genoplante  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplante' (<http://www.genoplante.com>  
and <http://genoplante-info.infobiogen.fr>).

FEATURES  
source  
1..657  
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Query Match 34.1%; Score 367.2; DB 14; Length 657;  
Best Local Similarity 80.8%; Pred. No. 1.3e-94;  
Matches 496; Conservative 0; Mismatches 98; Indels 20; Gaps 5;  
QY 1 ATGGCTACCTCAAGCATGAAGAGCATTC---AATGGGATCCCAAGTTTCTCATGTGT 57  
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DB 111 CACAAGCAGAGCTCCTCAAGGAAGAAGGCAAAAGCCGAGACCCGAGCCCAAGAGAA 170  
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QY 172 GGATGGAGAACTCGTTTACTTACTATTCAAGGTTTGGTCCGAGCAAGAGATT 231  
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DB 411 CACCGTTTGTATCCGGT-----TCTGACCACTCTCTCTCATCACTCAACCTCTCAT 461  
QY 412 GACCTTG-TACCTTTCTTCAGTACAAGCTTTACGCCAAGGAGATTTCCCATCTCTC 470  
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QY 590 TCTCTTCGTGGCAT 603  
DB 642 TCTCTCTCTGGCAT 655

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DEFINITION BOIGS48TF BO\_1.4\_1.6\_KB\_nuc Brassica oleracea genomic clone  
BOIGS48, genomic survey sequence.

CC952179  
ACCESSION CC952179.1 GI:33790676  
VERSION GSS

KEYWORDS Brassica oleracea  
SOURCE Brassica oleracea

ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica;  
1 (bases 1 to 760)

REFERENCE  
AUTHORS Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.

TITLE  
JOURNAL  
COMMENT  
Whole genome shotgun sequencing of Brassica oleracea  
Unpublished (2001)  
Other GSSs: BOIGS48TR  
Contact: Chris Town

TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA.  
Tel: 301-838-3523  
Fax: 301-838-0208  
Email: cdtown@tigr.org  
DNA is from a doubled haploid provided by Tom Osborn.  
Seq primer: TF  
Class: sheared ends.

FEATURES  
Location/Qualifiers  
1..760

/organism="Brassica oleracea"  
/mol\_type="genomic DNA"  
/strain="TO1000DH3"  
/db\_xref="taxon:3712"  
/clone="BOIGS48"  
/clone\_lib="BO\_1.4\_1.6\_KB\_nuc"  
/note="Vector: PHOS2; Site 1: BstXI; 1.4-1.6 kb sheared  
nuclear DNA inserted into PHOS2 using BstXI linkers"

## ORIGIN

Query Match 34.0%; Score 365.8; DB 29; Length 760;  
Best Local Similarity 81.0%; Pred. No. 3.4e-94;  
Matches 469; Conservative 0; Mismatches 92; Indels 18; Gaps 3;  
QY 1 ATGGCTACCTCAAGCATGAAGAGCATTC---AATGGGATCCCAAGTTTCTCATGTGT 57  
DB 570 ATGGCGACCTCAAGCATCAAGAGTGTTCCTCAATATATGGCATCCCAAGTTTATCCATTGC 511  
QY 58 CACAAGCTCGAGCTCCTTAAAGAGGCAAACTCGCGACGTCCCGA-----AAGCCGAA 111  
DB 510 CACAAGCAGAGCTCTCTCAAGAGAGGCAAAAGCCGAGACCCGAGCGCCCAAGAGAA 451  
QY 112 GAAGATGAAGGCTAAGCTGCGAGTTCAAGAGATGTGGATTCTCTTCTTAAGAGAGA 171  
DB 450 GAAGAAGAAGGCTAAGCTACGAGTTCTTAGAGATGTGGACTCTCTTCTTAAGAGAGA 391  
QY 172 GATCGAGAACTCGTTTACTTACTTATTCGAAGGTTTTCGTCGCAAGCCCAAGAGATT 231  
DB 390 GGTGGAGAACTCGTCATCTTTACTGTTTCAAGCTTTTGTGTCGCAAGCCCAAGAGATT 331  
QY 232 CAAGCCATCATGTCTTTTCCAAAAACATTTCCAATCCCTCGAAAAACGAGCTGTTCTCGCC 291  
DB 330 CATGCCATCATGTCTCTTCCAGAAACATTTCAAGCTCTTCCAAAGATGTTATCTTGTCT 271  
QY 292 ACCATACCTAAATCCGGTACAACTGGCTAAAGCTTTAAGCTTTTCACTTCAACCTTAAACCGT 351  
DB 270 ACCATACCAAAATCCGGTACAACTGGTTAAAGCTTAAAGCTTTTACCTCTTAAACCGA 211  
QY 352 CACCGTTTGTATCCGGTTGCTCGAGTACCAACCACTCTTTTCACTTCCAAACCTCTCAT 411  
DB 210 CACCGTTTGTATCCGGT-----TCTGACCACTCTCTCTCATCACTCAACCTCTCAT 160  
QY 412 GACCTTGATCTTCTTCGAGTACAAGCTTTACGCCAAGGAGATGTTCCGATCTCTCG 471  
DB 159 GACCTCGTACCTTTCTTGGAGTACAAGCTTTTACGCCAAGGAGATGTTCTGTATCTCTCC 100  
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DB 39 ATCGAGGAACCGGAGTGAAGAAAGTACTTGTGTCGG 1

Search completed: August 17, 2004, 05:07:02  
Job time : 3232 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 17, 2004, 02:51:44 ; Search time 97 Seconds  
(without alignments)  
6161.671 Million cell updates/sec

Title: US-10-019-931-1

Perfect score: 1077

Sequence: 1 atggctacctcaagcatgaa.....gtctcactttcagggttgagc 1077

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.\*

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3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	47.6	4.4	7218	1	US-08-232-463-14
3	35.8	3.3	1236	2	US-08-741-134-5
4	34.2	3.2	474	4	US-09-621-976-18033
5	33.8	3.1	474	4	US-09-621-976-18033
6	33.8	3.1	12720	1	US-08-403-866-11
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8	32.4	3.0	3910	4	US-09-302-6208-91
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11	31.6	2.9	11303	4	US-08-961-527-115
12	31.4	2.9	756	3	US-09-013-067A-7
13	31.4	2.9	2572	4	US-09-489-847-44
14	31.4	2.9	6794	4	US-09-491-356C-2
15	31.2	2.9	828	4	US-09-107-532A-359
16	31.2	2.9	828	4	US-09-134-000C-3123
17	31.2	2.9	9636	1	US-08-323-170B-1
18	31.2	2.9	9636	1	US-08-954-441-1
19	31.2	2.9	1330025	4	US-09-198-452A-1
20	31.2	2.9	4403765	3	US-09-103-840A-2
21	31.2	2.9	4411529	3	US-09-103-840A-1
22	31	2.9	505	4	US-09-621-976-15639
23	30.8	2.9	3826	4	US-09-302-6208-90
24	30.8	2.9	3826	4	US-09-912-161-13
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27	30.6	2.8	5304	4	US-09-023-655-664

Query Match 4.5% ; Score 48 ; DB 1 ; Length 7218 ;

#### ALIGNMENTS

##### RESULT 1

US-08-232-463-14  
; Sequence 14, Application US/08232463  
; Patent No. 5670367  
; GENERAL INFORMATION:  
; APPLICANT: DORNER, F.  
; APPLICANT: SCHEIFLINGER, F.  
; APPLICANT: FALKNER, F. G.  
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 1800 Diagonal Road, Suite 500  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22313-0299  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/232,463  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/935,313  
; FILING DATE:  
; APPLICATION NUMBER: EP 91 114 300.6  
; FILING DATE: 26-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)836-9300  
; TELEFAX: (703)683-4109  
; TELEX: 899149  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7218 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; CLONE: pTZ9pt-F18  
US-08-232-463-14

Sequence 296, App  
Sequence 4884, App  
Sequence 8976, App  
Sequence 292, App  
Sequence 4830, App  
Sequence 294, App  
Sequence 4859, App  
Sequence 280, App  
Sequence 4842, App  
Sequence 272, App  
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Sequence 327, App

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1095 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1154
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325 GCTTTAATCTTACCATCTCTTAACGTACCGGTTTGATCCGGTGCCTCGAGTACCAAC 384
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1155 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1214
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385 CACCCTCTTTTCATCTCCACACCTCATGACCTTGACCTTCTTCGTAGTACAGCTTAC 444
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1215 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1274
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445 GCCAACGGAGATGTTCCGATCTCTCGGCTAGCCAGTCCAAGAACGTTGCAACCCAC 504
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1275 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1334
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505 TTACCGTTTCGGTTCCTTAAGGAAACGATCGAGAAACCCGGTGTGAAGTCGTACTTG 564
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565 TGCCGGAAACCGGTTTGACATCTCTTCGTGGCATTACCAACACATCAA 620
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1395 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYGGPACAAATTCCTA 1450
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```

TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,463  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
PRIOR APPLICATION NUMBER: US/07/935,313  
FILING DATE:  
APPLICATION NUMBER: EP 91 114 300.6  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)836-9300  
TELEFAX: (703)683-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:

RESULT 2  
US-08-232-463-14/c  
; Sequence 14, Application US/08232463  
; Patent No. 5670367  
; GENERAL INFORMATION:  
; APPLICANT: DORNER, F.  
; APPLICANT: SCHEIFLINGER, F.  
; APPLICANT: FALKNER, F. G.  
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 1800 Diagonal Road, Suite 500  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22313-0299  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/232,463  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/935,313  
; FILING DATE:  
; APPLICATION NUMBER: EP 91 114 300.6  
; FILING DATE: 26-JUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 304772/114 IMMU  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)836-9300  
; TELEFAX: (703)683-4103  
; TELEX: 899149  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:

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; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-2090
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1236 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: not relevant
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1236
; US-08-741-134-5

Query Match          3.3%; Score 35.8; DB 2; Length 1236;
Best Local Similarity 51.6%; Pred. No. 0.07; 77; Indels 0; Gaps 0;
Matches 82; Conservative 0; Mismatches 77;

QY 791 AGACCAACTGAAGAGCTGCAACTTCTTAGAGCTTCCTTACCGAAGAGAGAAC 850
DB 525 AGACGAAGATGAGAGCGTGACATCTATGACAGTGAAGACTACGACTTGACCCAGATGA 584
QY 851 GAAGGGAGTGTGAAGGCTATCCCGAGCTGTGTAGCTTCGAGAACTCGAAGAGTTGG 910
DB 585 GGATGAATATTGGCGACGACATCGGACGACTTGGATGCGAAGAGGAAGAAGTTCG 644
QY 911 AGGTGAACAAGTCAACAAGTCGATCAAGAACTTTGAGA 949
DB 645 TATTGAAGAAGTCCACGAAGAAGATGAAGAATAATGA 683

RESULT 4
US-09-621-976-18033
; Sequence 18033, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 18033
; LENGTH: 474
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 16
; OTHER INFORMATION: n=a, g, c or t
; US-09-621-976-18033

Query Match          3.1%; Score 33.8; DB 4; Length 474;
Best Local Similarity 14.0%; Pred. No. 0.18;
Matches 42; Conservative 131; Mismatches 123; Indels 3; Gaps 1;

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DB 320 MYRRGGKYRRRAARRWTWARRAATYTWYTKWGSCKWKSMMRKRKYMCKCYWWR 261
QY 653 AAGCTTTTGAATCTGATTGTCGGGGAGTCAATCGGGTTTGGCCCGTTTGGGAACACATGT 712
DB 260 KYCCMRKKRRRGGKRRARSYKSGYKGGSYTYKGGKGGTGGKGVAMSKGRRAMTTT 201
QY 713 TGGGATCTGGAGAGAGAGCTTGAAGAGACACAGAAAGTCTTCTTTTAAGGTAGAGG 772
DB 200 YYYKKKW---RSYWAARGTKTKKWAAMMMCMWYMRSMYMYKKWAAAWKSCCMARK 144
QY 773 ATCTCAAGACGACATCGAGACCAACTTGAAGAGGCTTGAACACTTCTTAGAGCTTCTT 832
DB 143 KGSSSGRWYMKRGCTCMGRRRWYRMRMCMWYCTKGSMAAMMSGKRAAMCCCKYY 84
QY 833 TCACCGAAGAGAGAGGAAGAAAGGGAGTTGTAAGGCTATCGCCGAGCTGTGTAGCTTC 891
DB 83 TWMCMAAAAMWMTWAAAAAAMMRSCGRMSKKKKGSRGSSSCYKSMRKYCCMRSYWM 25

RESULT 6
US-08-403-866-11
; Sequence 11, Application US/08403866
; Patent No. 5643779
; GENERAL INFORMATION:
; APPLICANT: Ehrlich, Stanislaw
; APPLICANT: Godon, Jean-Jacques
; APPLICANT: Renault, Pierre
; TITLE OF INVENTION: Nucleic acid coding for an alpha-acetolactate
; TITLE OF INVENTION: synthase from Lactococcus and its applications
; NUMBER OF SEQUENCES: 16
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICANT NUMBER: US/08/403,866
; FILING DATE:
; CLASSIFICATION: 435
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DB 371 GWTAAWACTKTCTGTGAAAATGTCTCATGTCTGTGTAATCCAGCA 415

RESULT 5
US-09-621-976-18033/c
; Sequence 18033, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 18033
; LENGTH: 474
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 16
; OTHER INFORMATION: n=a, g, c or t
; US-09-621-976-18033

Query Match          3.1%; Score 33.8; DB 4; Length 474;
Best Local Similarity 14.0%; Pred. No. 0.18;
Matches 42; Conservative 131; Mismatches 123; Indels 3; Gaps 1;

QY 593 CTTCTGGCATTACACCAACATCAATCCGAGTCAGTCAGCCAGCTTGTGTAGACC 652
DB 320 MYRRGGKYRRRAARRWTWARRAATYTWYTKWGSCKWKSMMRKRKYMCKCYWWR 261
QY 653 AAGCTTTTGAATCTGATTGTCGGGGAGTCAATCGGGTTTGGCCCGTTTGGGAACACATGT 712
DB 260 KYCCMRKKRRRGGKRRARSYKSGYKGGSYTYKGGKGGTGGKGVAMSKGRRAMTTT 201
QY 713 TGGGATCTGGAGAGAGAGCTTGAAGAGACACAGAAAGTCTTCTTTTAAGGTAGAGG 772
DB 200 YYYKKKW---RSYWAARGTKTKKWAAMMMCMWYMRSMYMYKKWAAAWKSCCMARK 144
QY 773 ATCTCAAGACGACATCGAGACCAACTTGAAGAGGCTTGAACACTTCTTAGAGCTTCTT 832
DB 143 KGSSSGRWYMKRGCTCMGRRRWYRMRMCMWYCTKGSMAAMMSGKRAAMCCCKYY 84
QY 833 TCACCGAAGAGAGAGGAAGAAAGGGAGTTGTAAGGCTATCGCCGAGCTGTGTAGCTTC 891
DB 83 TWMCMAAAAMWMTWAAAAAAMMRSCGRMSKKKKGSRGSSSCYKSMRKYCCMRSYWM 25

RESULT 6
US-08-403-866-11
; Sequence 11, Application US/08403866
; Patent No. 5643779
; GENERAL INFORMATION:
; APPLICANT: Ehrlich, Stanislaw
; APPLICANT: Godon, Jean-Jacques
; APPLICANT: Renault, Pierre
; TITLE OF INVENTION: Nucleic acid coding for an alpha-acetolactate
; TITLE OF INVENTION: synthase from Lactococcus and its applications
; NUMBER OF SEQUENCES: 16
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICANT NUMBER: US/08/403,866
; FILING DATE:
; CLASSIFICATION: 435
```



87	MMVMYNGWRSSYMAWTRTWGTYAYRSMMYWWRYRCWKKKAYYRKTKTCYSSKGTWTKR	146
Db		

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; TITLE OF INVENTION: THERETO
; FILE REFERENCE: M6368 (1010-35)
; CURRENT APPLICATION NUMBER: US/09/912,161
; CURRENT FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 14
; LENGTH: 3910
; TYPE: DNA
; ORGANISM: Candida tropicalis
US-09-912-161-14

Query Match      3.0%; Score 32.4; DB 4; Length 3910;
Best Local Similarity 54.1%; Pred. No. 2.6;
Matches 66; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 883 TGTAGCTTCGAGATCTGGAAGTTGGAGTGCAACAGTCAACAGTCGATCAAGAAC 942
Db 3718 TCGGCTCTGTGTGCAAGAAGTCTTCGATGAATCTGTTGAAGATGTCGATCTCG 3659

QY 943 TTTGAGAAATCGATTCTTTGTTTCGGAAGAGGAGAGTGAGTGATTTGGTTAACTATTGTC 1002
Db 3658 TCCAAGTGTGCTTGTGTTGTTCTGGAAGCCCAAGTTGATCAAGCCCGTGGTCAACTTCTCA 3599

QY 1003 CC 1004
Db 3598 CC 3597

RESULT 10
US-09-313-294A-6743/C
; Sequence 6743, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 6743
; LENGTH: 285
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700352328H1
US-09-313-294A-6743

Query Match      3.0%; Score 32.2; DB 4; Length 285;
Best Local Similarity 57.4%; Pred. No. 0.46;
Matches 58; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 574 CCGTTTCACATTCATCTCTCTGTCGATTACACCAACATCAATCCGAGTCAGTG 633
Db 109 CCGTTTGACATCCACATCAACAGGAGGATCGATCGACCAATCCAGGTTTTT 50

QY 634 AGCCAGTCTTGCTAGACCAAGCTTTTGATCTGTTATTCGCG 674
Db 49 AGCAATCTGTGTAAGCATATCTTTTATGTATGCAATTCG 9

RESULT 11
US-08-961-527-115/c
; Sequence 115, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: P3340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11303 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-115

Query Match      2.9%; Score 31.6; DB 4; Length 11303;
Best Local Similarity 54.2%; Pred. No. 11;
Matches 64; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 883 TGTAGCTTCGAGATCTGGAAGTTGGAGTGCAACAGTCAACAGTCGATCAAGAAC 942
Db 8207 TGTACTTTAAGCAATTTGAAGAGGCTGTTCTAAAGCAGGAAACCACTTGACAAATAC 8148

QY 943 TTTGAGAAATCGATTCTTTGTTTCGGAAGAGGAGTGAGTGATTTGGTTAACTATTGTT 1000
Db 8147 CTCCTCAGCCTATATTCCTATTCATCCATGGGAATTGAAAATGCTAATTTGATTCT 8090

RESULT 12
US-09-013-067A-7
; Sequence 7, Application US/09013067A
; Patent No. 6057144
; GENERAL INFORMATION:
; APPLICANT: TOKOYASU, KEN
; APPLICANT: MORI, YUTAKA
; APPLICANT: HAMATSU, SHIOKA
; APPLICANT: HAYASHI, KIYOSHI
; TITLE OF INVENTION: CHITIN DEACETYLASE GENE, VECTOR CONTAINING
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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/ APPLICATION NUMBER: US/09/013_067A
/ FILING DATE: 01-JAN-1998
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP 9-345737
/ FILING DATE: 02-DEC-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: OBLON, NORMAN F.
/ REGISTRATION NUMBER: 24,618
/ REFERENCE/DOCKET NUMBER: 8361-0002-0
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 703-413-3000
/ TELEFAX: 703-413-2220
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 756 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "PCR REACTION PRODUCTS"
/ ORIGINAL SOURCE:
/ ORGANISM: Colletotrichum lindemuthianum
/ STRAIN: ATCC 56676
/ US-09-013-067A-7

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	Query Match	2.9%;	Score 31.4;	DB 3;	Length 756;
	Best Local Similarity	54.9%;	Pred. No. 1.8;		
	Matches 62;	Conservative 0;	Mismatches 51;	Indels 0;	Gaps 0;
QY	338	CAATCTTAACCGTCACCGGTTGATCCGGTTCCTCGAGTACCAACCAACCTCTTTTCA	397		
Db	107	CAATCTTCAGTGCACCGACCGCTGGTCTGCTGACCTACGACGCGTCTCTTTCA	166		
QY	398	CTTCCAAACCCCTCATGACCTCTGTACTCTTCTTCGAGTACAAAGCTTTACGCCAAC	450		
Db	167	CTTTTCACCGCTCAAGCTCTCTCGAATCTTTGAAGCAGAACGACGCTCAAGGCGACC	219		

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RESULT 13
US-09-489-847-44
; Sequence 44, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: PZ031PI
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44
; LENGTH: 2572
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2527)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-489-847-44

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	Query Match	2.9%;	Score 31.4;	DB 4;	Length 2572;
	Best Local Similarity	53.7%;	Pred. No. 4.3;		
	Matches 65;	Conservative 0;	Mismatches 56;	Indels 0;	Gaps 0;
QY	863	TGAAGGCTATCGCGGAGCTGTGTAGCTTCGAGAACTCTGAAGAAGTTGGAGGTGAACCAAGT	922		
Db	854	TGTCGCGATCGCTGGTGGTGTATCTTACCGGAAGCAGAAAGAAGATCGAGAAATGAGT	913		
QY	923	CAAAACAAGTCGATCAAGAAGCTTTTGAGAATCGATTCTTGTTTCGGAAGGAGAGAAGTGGAGTG	982		
Db	914	CGGCCACGAGGGGGGAAGACTCTGCCATGACAGACATCGCTCCGACAGAGGAGGTGCACAG	973		
QY	983	A	983		
Db	974	A	974		

```

RESULT 14
US-09-491-356C-2
; Sequence 2, Application US/09491356C
; Patent No. 6566061
; GENERAL INFORMATION:
; APPLICANT: Philibert, Robert A.
; APPLICANT: Ginns, Edward I.
; APPLICANT: Delisi, Lynn
; TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF X013
; FILE REFERENCE: 9465.6US11
; CURRENT APPLICATION NUMBER: US/09/491,356C
; CURRENT FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: PCT/US99/09365
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/083,465
; PRIOR FILING DATE: 1998-04-29
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 6794
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-491-356C-2

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	Query Match	2.3%;	Score 31.4;	DB 4;	Length 6794;
	Best Local Similarity	48.6%;	Pred. No. 8.8;		
	Matches	86;	Conservative 0;	Mismatches 91;	Indels 0; Gaps 0;
Qy	777	CAAGAAGCAGCATCGAGACCAACTTTGAGAGGCTTGCAACTTTCTTGAAGCTTCCTTTCAC	836		
Db	4722	CACGTGCGACATGCACTGCGCAACAATGAGCTTTCACCTGTGTTGGACATGCTGAGCGT	4781		
Qy	837	CGAAGAAGAGGAAACGAAAGGGAGTTGTGAAGGCTATCGCGAGCTGTGAGCTTTCAGAA	896		
Db	4782	GCTCATCAATGGACATTTGGCTCGACACATGCTACGCTCTCGCRAAGTAGCATGAGGA	4841		
Qy	897	TCTGAAGAAGTTGGAGGTGAACAAGTCAACAACAAAGTCGATCAAGAACTTTGAGAAATCG	953		
Db	4842	AAACAAGCGTGCATACATGAACCTGGCGAAGAAGTTGCAGAAGGAGCTTGGGGAGCG	4898		

RESULT 15  
 US-09-107-532A-359  
 ; Sequence 359, Application US/09107532A  
 ; Patent No. 6583275  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lynn A Doucette-Stamm and David Bush  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
 ; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
 ; NUMBER OF SEQUENCES: 7310  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSES: GENOME THERAPEUTICS CORPORATION  
 ; STREET: 100 Beaver Street  
 ; CITY: Waltham  
 ; STATE: Massachusetts  
 ; COUNTRY: USA

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;
;
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
;
; INFORMATION FOR SEQ ID NO: 359:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 828 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3) LOCATION 1...828
; SEQUENCE DESCRIPTION: SEQ ID NO: 359:
;
US-09-107-532A-359
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Query Match      2.9%; Score 31.2; DB 4; Length 828;
Best Local Similarity 48.3%; Pred. No. 2.3;
Matches 87; Conservative 93; Indels 0; Gaps 0;

Qy 155 CTCCTCCTAAGGAGAGGATGGAGAACTCGTTACCTTTACCTATTCCAAAGGGTTTGGT 214
Db 398 CTGTTATGGCGCATATAGGTTTAAACCTCAATCTGTTAATGCAATTTGGAGATTAAAG 457
Qy 215 GCCAAGCCAAAGAGATCAAGCCATCATGCTTTCCAAAACATTTCCCAATCCCTCGAAA 274
Db 458 TACAGAGAGAGCAAGAGAGCTCTAAAGATTAAAGAGCTGCTAAAGCTGTAGAAA 517
Qy 275 ACGACGTGTTCTCGCCACCACCTAAATCCGTCACAACTGGCTAAAGCTTTAACTT 334
Db 518 AAGCAGGAGCATTCGCTGTAGTGTAGATGTGTTCCAACTAAGCTTGCAGAGTTAATT 577
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Search completed: August 17, 2004, 05:09:07  
Job time : 122 secs

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Db 167 AGTTGGAGAACACGTTATATATATCTATTTCAAGGATTTTGGTGCAGGCATTTGGAAT 226  
Qy 231 TCAGCCATCATGCTTTCCAAAACATTTCCATCCCTCGAAAACGACGTGTTCTCGC 290  
Db 227 CCAAGCAATATCACTTTGAGAGCACTTCCAGCTTAAGACAGTGTATTTGGC 286  
Qy 291 CACCATACCTAAATCCGGTCAACCTGGCTAAAGCTTTAACTTTCCATCCCTTAACCG 350  
Db 287 CACAATCCAAAATCAGGTACCTTGGCTGAAAGCTCTCACCTTTGCCATTTGCAATCG 346  
Qy 351 TCACGGTTTGCATCCGGTGGCTCGAGTACCAACACCTCTTTTCACTTCCACCTCA 410  
Db 347 CCATCTCATAGTATCACTACATCAATGTCTCATCTTTGCTTACTTCTATCTCTCA 406  
Qy 411 TGACCTTGTACTTTCTTCGAGTACAGCTTTTACGCCAACG-----GAGATGTTCCCGA 464  
Db 407 TGAATCTGTGCTTTTATAGATACACCGTTTATGGTAATGCCCTAGCCATGTTCCAAA 466  
Qy 465 TCTCTCGGCTAGCCAGTCCAGAACGTTCCGAAACCACTTACCGTTCGGTCCCTAAA 524  
Db 467 CCTATCCAAATGACTGAGCCAAAGACTTTTGGTACACATATTCATTCATGCAITGGC 526  
Qy 525 GMAACGATCGAGAAACCCGGTGTGAAGGTGCTGTACTTGTGCCGGAACCCGTTTGACAC 584  
Db 527 CAAGTCCATCAAGGAGTCCATAGTAGAATAATTTATATATGTAGGAACCCACTTGAC 586  
Qy 585 ATTCAATCTCTCGTGGCATATACCAACCAACATCAATCCAGTTCAGTACGACCGACTT 644  
Db 587 TTTTGTGTCTATTGGATTTTCTCAACAAAATTAAGCCAGAACATTTACTGAAATTTGA 646  
Qy 645 GCTAGACCAAGCTTTTGTATGTTGCGGGAGTGTATCGGTTTGGCCGCTTTTCGGGA 704  
Db 647 ACTAGGGAGCTTTTGAAGATTTGCAAGAGATTAATAGGGTTTGGTCCAACTTGGGA 706  
Qy 705 ACACATGTTGGGATCTCGAGAGAGAGCTTGAAGAGACCAAGAGAAAGTCTTTTAAAG 764  
Db 707 CCAATGTTGGTTATTGGAAGGAGATATAGTAGGCTTAGTAAGGTTTGTCTTTGAA 766  
Qy 765 GTACGAGATCTCAAGACGACATCGACCACTTGAAGAGGCTTGCACCTTTCTTGA 824  
Db 767 GTACGAGATCTTAAAGAGATGTCATTTTCATGTGAAGAAATAGCGAGTCTTAGG 826  
Qy 825 GCTTCTTCCCGAAGAGAGAACGAAAGGAGTTGTGAAGCTATCGCCGAGCTGTG 884  
Db 827 ATGTCCTTTCATTCGGAGGAGAGAGTGTAGGACTATTGAGAGCAATAATCAAGCTATG 886  
Qy 885 TAGCTTCAGAAATCTGAAGAGTTGGAGGTGAACAGTCAACAAAGTCGATCAAGACTT 944  
Db 887 CAGCTTCGAGAAGATGAAGGAATTTGGAGGCAATAAATCTGGAACATTTGCTAGGAACCT 946  
Qy 945 TGAGATCGATCTTTGTTTCCGAAGAGAGAGTGAATGAGTGGGTAACTATTGTTCACC 1004  
Db 947 TGAGAGAAAGTACTTTTCCGAAGGCTGAATGGAGATTGGTGAATCTTCCCTTCCC 1006  
Qy 1005 TTCAGAGTGAAGATTTGTCAGCTTGTAGTGAACAGTGAAGTGAATGCTGTCTCAC 1064  
Db 1007 TGAATGGGTGAAGATTTATCCAAATTTATGGAAGAAAGTTAAGTGGGTGAGCTTGTG 1066  
Qy 1065 TTT 1067  
Db 1067 ATT 1069

## RESULT 2

US-09-938-842A-2049  
; Sequence 2049, Application US/09938842A  
; Patent No. US20020160378A1  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Kreps, Joel  
; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

; TITLE OF INVENTION: SAME, AND METHODS OF USE  
; FILE REFERENCE: SRIPI300-3  
; CURRENT APPLICATION NUMBER: US/09/938,842A  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/227,866  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/264,647  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/300,111  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 5379  
; SEQ ID NO 2049  
; LENGTH: 981  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-938-842A-2049  
Query Match 21.3%; Score 229.2; DB 9; Length 981;  
Best Local Similarity 54.9%; Pred. No. 2.3e-65;  
Matches 525; Conservative 0; Mismatches 413; Indels 18; Gaps 3;  
Qy 112 GAAGATGAAGGCTAAGCTGCGAGTTCCAAGAGATGTTGGATCTCTTCTTCTTAAGAGAGA 171  
Db 34 GGAGATGAAGATCTGACACAGAAAACAAGAGCTCTGATCTCTTCTTCTTCTTAAGAGAAA 93  
Qy 172 GGATGGAGAACTCGTTTACCTTTTACCTATTCCAAGGGTTTGGTGCCAAAGCCAAAGAGATT 231  
Db 94 GGTGGTAGTGAAGTGAATATATGAATTCAGAGACTTGGCACACACAAGCTATTTTA 153  
Qy 232 CAAGCCATCATGCTTTCCAAAACATTTCCAAATCCCTCGAAAACGAGAGTGTCTTCGCC 291  
Db 154 CAAGGAATCTTATCTGTCNAAGACGCTTTGAAGCTTAAGATTCGACATATTCCTCGTC 213  
Qy 292 ACCATACCTAAATCCGTTACACCTGGCTAAAGCTTTAACTTTTCCACCATCTTAAACCGT 351  
Db 214 ACTAATCTTAATCAGGTACCACTTGGTTTAAAGCTCTTGCTTTGCTCTCTTAAACGA 273  
Qy 352 CACCGGTTTGATCCGGTTGCTCGAGTACCAACCACTCTTTTCACTTCCAAACCTCAT 411  
Db 274 CACAAGTT---TCCAGTTTCTTCTTCTGTAAACCATCTCTTCTGTCAACCAATCCAC 330  
Qy 412 GACCTTGACCTTTCTCGAGTACAGCTTTACGCAAGAGAGATGTTCCGATCTCTCG 471  
Db 331 CTCTTGTCCTTCTTGGAGAGGATTTACTACGAGTCCCAGATTT---CGATTTCTCC 387  
Qy 472 GGTAGCCAGTCCAAAGAACGTTTCGAACCCCACTTACCGTTTCGGTTCCTTAAAGAAACG 531  
Db 388 AGTTGCTTCTTCCAGACTGATGAACAGCACATATCGCATCTTTCGCTCCCGAGTCT 447  
Qy 532 ATCGAGAAACCCGGTGTGAAGTCTGTGCTGTCGCGAACCCGTTTGACACATTCATC 591  
Db 448 GTTAAGAGCTCTCTTGTGAAGATTGTGTTTGTAGAACCCCTAAGGACATGTTTGTG 507  
Qy 592 TCTTCTGTCATTTACCAACCAACATCAATCCGAGTCACTGAGCCAGTCTTGTAGAC 651  
Db 508 TCTTATGAGCAATTTGGGAAAAGAGTAGCTCTCGAGAAACCGCGGATATTCATTCGA 567  
Qy 652 CAAGCTTTTGTATCTGTATTTGCGGGAGTGAATGCGGTTTGGCCGCTTTTGGGAAACATG 711  
Db 568 AAAAGGTTTGAAGCGTTTGTGAAGGGAAGTTTATAGGTGGACCCCTTTGGGATCATATA 627  
Qy 712 TTGGGATCTGGAGAGAGCTTGAAGAGACCAAGAGAGTCTTCTTTTAAAGTACGAG 771  
Db 628 TTGGAGTACTGATGCAAGCCGCGAGAAATCCGAACAGGTTTGTGTTTACTTACGAG 687  
Qy 772 GATCTCAAGAGACATCGAGACCACTTGAAGAGGCTTGAACCTTTCTTAGAGTCTCT 831  
Db 688 GAGCTAAAGAGACAGACCCGAGTGTAGATGAAGCGGATCGCGAGTCTTGTGAATGTGC 747  
Qy 832 TTCACCGAAGAGAGAACGAAGGGAGTTGTGAAGGCTATCGCGAGCTGTGTAGCTTC 891  
Db 748 TTATTGAAGAGAGAA-----GTGAGAGAGATTGTGAAGTTGTGTAGCTTT 795



Qy	892	GAGAACTCTGAAGAAGTTCGGAGTGAACAAAGTCAAAACAAAGTCGATCGATCAAGAAGCTTTGAGAA	951
Db	796	GAGAGTTTAAAGTAAATTCGGAAGTTAAACAAGAAGCGAAATTCGCAAAATGGAATGAGACT	855
Qy	952	CGATTCCTGTTTCGGAAGGAGAAGTGAAGTGGGTAACTATTTCTACCTTCACAA	1011
Db	856	AAAACTTTCTTTAGAAAAAGGAGAGATTCGAGAGTGGAGAGATCTTTGAGTGAGTCATTG	915
Qy	1012	GTGGAAGATTGTGAGCCCTTAGTGGATGACAAGTTAGGTAGTCTGGTCTCACTTT	1067
Db	916	GCAGAGGAAATTTGATAGAACCATTTGAAGAGAAAGTTTAAAGGTTCTGGTCTTAAATTT	971

### RESULT 3

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US-09-938-842A-2049
; Sequence 2049, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAVE, AND METHODS OF USE
; FILE REFERENCE: SCRI1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2049
; LENGTH: 981
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2049

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Query Match	21.3%;	Score 229.2;	DB 11;	Length 981;
Best Local Similarity	54.9%;	Pred. No. 2.3e-65;		
Matches 525; Conservative	0;	Mismatches 413;	Indels 18;	Gaps 3;

112	Qy	GAAGATGAAGGGCTAAGCTGCGAGTTCCAAAGAGATGTTGGATTTCTTCTCTTAAGGAGAGA	171
34	Db	GGAGATGAAGATCTGACACAAAGAAACAAGAGCTCTGATCTCTTCTCTCTTAAAGAGAAA	93
172	Qy	GGATGGAGAACTCGCTTACCTTTACCTATTCCAAAGGGTTTTGGTGGCCAAAGCAAGAGATT	231
94	Db	GGTTGGTTAGTAGTGAAATATATGAATTCCAAGACCTTTGGCACACACAAGCTATTTTTA	153
232	Qy	CAAGCCATCATGTCTTTCCAAAAACATTTCCAAATCCCTCGAAAAACGAGCTGGTTCTCGCC	291
154	Db	CAAGGAATCTTGATCTGCCAAAAACGCTTTGAAGCTAAAGATTCCGACATTTATCCTCGTC	213
292	Qy	ACCATACCTAAATCCGGTACAAACCTGGCTAAAGCTTTAATTTACACATCCTTAAACGT	351
214	Db	ACTAATCCTAAATCAGGTACACATTGGTTAAAGCTCTGTGCTTTGTCTCTCTTAAACGA	273
352	Qy	CACCGGTTTGATCCGGTGGCTCGAGTACCAACACACCTCTTTTCACTTCCCAACCCCTCAT	411
274	Db	CACAAGTT--TCCAGTTTCTTCTCTGGTTAACCATCCTCTCTTGGTCAACCATCCACAC	330
412	Qy	GACCTTGTAACCTTTCTTCGAGTACAAGCTTTACGCCAAAGGAGATGTTCCGATCTCTCG	471
331	Db	CTTCTTGTGGCCTCTTTGGAAGGAGTTTACTACGAGTCCCAGATT--CGATTTCTCC	387
472	Qy	GGTCTACCGAGTCCAAGACGTTTCGCACCACTTACGGTTCGGTTCCCTTAAAGAAACG	531
388	Db	AGTTTGGCTCTTCCAAGACTGATGAACACGCACATATCGCATTTTTCGCTCCCGAGTCT	447
532	Qy	ATCAGAGAAACCCGGTGTCAAGGTCGTGCTACTTTGTGCGGAAACCGGTTTGACATTTATC	591

Db	448	GTTAAGAGCTCGTCTTTGTAAGATTGTGTATTGTGTAGGAACCCCTAAGGACATGTTTGTG	507
Qy	592	TCCTTCGGCGATTACACCAACACAAATCCGAGTCAGTGAGCCAGTCCTGCTAGAC	651
Db	508	TCCCTTATGGCATTTTGGGAAAAGAGCTAGCTCCCTGAGGAAAACCGGGGATTATCCTATCGAA	567
Qy	652	CAAGCTTTTTCATCTGTATTCCCGGGGAGTGATCGGGTTTGGCCCGTTTTTCGGGAACACATG	711
Db	568	AAAGCGGTTCGAACGTTTCTGTAAGGGAAGTTTATAGGTGACCCCTTTTCGGATCATATA	627
Qy	712	TTGGGATACCTGGGAGAGAGAGCTTGAAGAGACCAAGAAAGTCCTCTTTTTTAAGGTACGAG	771
Db	628	TTGGAGTACTGTGTTATGCAAGCCGCGAATCCGAAACAAGGTCCTGTTGTTTACTTACGAG	687
Qy	772	GATCTCAAGACGACATCGAGACCAACTTGAAGAGGCTTGCACATTTCTTTAGAGCTTCCT	831
Db	688	GAGCTAAAGAAACAGACCCGAAGTTGAGATGAACGGATCGCGAGTTCTTTGGAATGTGC	747
Qy	832	TTCCCGAAGAAAGAGGAACGAAAGGGAGTTGTGAAGGCTATCGCCGAGCTGTGTAGCTTC	891
Db	748	TTTATTGAACAAGAA-----GTGAGAGAGATTGTGAAGTTGTGTAGCTTT	795
Qy	892	GAGMACTGGAAGTTGGAGGTGAACAAGTCAAAACAAGTCGATCAAGAAGCTTTGAGAAT	951
Db	796	GAGAGTTTAAAGTAATTGGAAGTTTAAACAAGAAGGGAAATTTGCCAAATGGAATAGAGACT	855
Qy	952	CGATTCTTGTTCGGAAGAGAGAAGTGAGTGAATTGGTTAACTATTGTCACTTCACCA	1011
Db	856	AAACATTCTTTAGAAAAGAGAGATTGGAGGATGAGAGATACCTTTGAGTGAGTCAATTG	915
Qy	1012	GTGAAAAGATTGACGCTTAGTGAGTGAACAAGTTAGGTGGATCTCGTCTCACTTT	1067
Db	916	GCAGAGGAAATTGATAGAACCAATTGAAGAGAAAGCTTTAAAGGTTCTGGCTTAAATT	971

## RESULT 4

```

US-10-424-599-82242
; Sequence 82242, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yonghui
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 82242
; LENGTH: 787
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_45281C.1
US-10-424-599-82242

```

	Query Match	20.6%	Score 221.8;	DB 13;	Length 787;
	Best Local Similarity	58.2%;	Pred. No. 5.9e-63;		
	Matches 435;	Conservative	0;	Mismatches 297;	Indels 15; Gaps 2;
Qy	104	AAAGCCGAAGAAGATGAAGGCTAAAGTCGGAGATTCCAAGAGATGTGGATTCTCTTCCTTA	163		
Db	50	AAGCAAGTGAAGAAACAAATTAAGCCAGATGTGAAGAGTTAATCTATCTCTTCCTTA	109		
Qy	164	AGAGAGAGATGGAGAACTCGTTACTTTACCTATTCCAAGGTTTTGGTGCCAAAGCCA	223		
Db	110	GAGAGAAGGTTGGATAACCGTATCTCTATTATTTCCAAGGCTTTTGGTACTCATCA	169		
Qy	224	AAAGAGATTCAAGGCATCATGTCTTTCCAAAACATTTCCAATCCCTCGAFAAGAGCTCG	283		

Dd 170 CTGAATCCAGCCATATAACACTTTTCAAAACCAATTCCTAGCTAAGGAGCAATGATGTTG 229  
Qy 284 TTCTGGCCACCATACCTTAATCCGGTACACCTGGCTAAAGCTTTAACTTTACCCATCC 343  
Dd 230 TTAATGCTAGTGTTCCTAAATCGGGACCACTTGGTTGAAAGCCCTTACCTTTGCTATTC 289  
Qy 344 TTAACCGTCCAGGTTTGGATCCGGTGTCTCGAGTACCAACCCCTCTTTTCACTTCCA 403  
Dd 290 TCCATCGCCAGTATTTCTCTCTAG-----AGAACCCACCTATTACTTATTTTCA 340  
Qy 404 ACCCTCATGACCTTGTACCTTTCTCGAGTACAAAGCTTTAG-----CCTAAGGAGATG 457  
Dd 341 ATCCCATGAATCTGTGCTCCATTTGAATTTGTCAATTTATGATGAATTAATGGCCAAA 400  
Qy 458 TTCCGGATCTCTGGGTACCGAGTCCAGAAAGTTTCGAACCCACTTACCGTTCCGGTT 517  
Dd 401 CTGATGACCTATCCAAATGCCAGGCCAAGAAATTTTGGGACTCATGTTCCCATTCATT 460  
Qy 518 CCCTAAAGGAAACGATCCAGAAACCCGGTGTGAAGGTGCTGTACTTGTGCGGAAACCCGT 577  
Dd 461 CATTTGCCCAATCAATTAAGAGACTGACTGTAGATCAATTTATTTGTAGGAATCTAT 520  
Qy 578 TTGACATATCATCTCTTCGTGGCAATTAACCAACACATCAAAATCCGAGTCAGTGAGCC 637  
Dd 521 TTGACACCTTTGTTTCTACTTTGGTTTTGTCAACAAATTTATGCCAAAGTTTGTGCTA 580  
Qy 638 CAGTCTCTAGACCAAGCTTTTGATCTGTATTCGGGGAGTGTATCGGGTTTGGCCCGT 697  
Dd 581 CATTAACCTCTAGAGAACTTTTGAAGATCTGTGAAGGATTAATTTGGCTTTGGTCCAT 640  
Qy 698 TTGGGAACACATGTTGGATCTGTGAGAGAGCTTTGAAGAGACCCAGAGAAAGCTTTCT 757  
Dd 641 CTGGAACCATATAGTATTAATTTGGAAGAGAGCAATTTGTAGGCCGGAAGAAAGTTTGT 700  
Qy 758 TTTAAGTACGAGATCTCAAGACGATCGAGACCACTTCAAGAGGCTTCAACTT 817  
Dd 701 TCTGAAGTACGAGACCTTGAAGAAATGTTCAATTTAATGTCGAAGAAATAGCTGAGT 760  
Qy 818 TCTTAGAGCTTCTTTACCGAAGAG 844  
Dd 761 TCTTGGTTGTCCTTCACTAAAGAG 787

## RESULT 5

US-09-938-842A-1027  
; Sequence 1027, Application US/09938842A  
; Patent No. US20020160378A1  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Kreps, Joel  
; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
; FILE OF INVENTION: SAME, AND METHODS OF USE  
; FILE REFERENCE: SCRIPI300-3  
; CURRENT APPLICATION NUMBER: US/09/938,842A  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/227,866  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/264,647  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/300,111  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 5379  
; SEQ ID NO 1027  
; LENGTH: 996  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-938-842A-1027

## Query Match

20.4%; Score 219.2; DB 9; Length 996;

Best Local Similarity 53.0%; Pred. No. 5.1e-62;

Matches 520; Conservative 0; Mismatches 453; Indels 9; Gaps 2;

Qy 86 AAATCGCGAGCTCCGAAAGCCGAAAGATGAAGGGCTAAGTTCGAGTTCACAGAGA 145  
Dd 17 AAGCTCATCACTTCCAAACTACATGAAGAGCGACAAGTGTAGTCAAGAACCAAGAACT 76  
Qy 146 TGTGGATTTCTTCTCTAAGGAGAGAGATGGAGAACTCGTTACCTTTACCTTATTCAG 205  
Dd 77 TGAATCATCTCTAAGTTCAGACAAAGATTTTATGGTCTCTACAACTACAAAG 136  
Qy 206 GCTTTTGGTCCAAAGGAGATTCAGGCATCATGCTTTCCAAACCAATTTCCAAAT 265  
Dd 137 GTTGTGGTACTATCCAAACACACTCCAAAGCGCTTTCAGCTCCAAACCACTTCAGC 196  
Qy 266 CCCTCGAAGAACGACGCTGTTTCGCGCACCATACCTTAATTCGCGTACAACTGGCTTAAAG 325  
Dd 197 CAGGAGATCTGATATAATCTCTCGCTTTTTCGCCAAAGGTGGAACCACTTGGCTCAAAT 256  
Qy 326 CTTTAACTTTCAACATCTTAACCTCACCCTGCTTTCGCGTTCGCTCGCTCGCTCGCT 385  
Dd 257 CCTTAATTTTCGCTGTTGTACATAGAGAAAGT-----ACGCGGAACCCCTCAAAC 310  
Qy 386 ACCCTCTTTTCACTTCCAAACCTCATGACCTTGTATCTTTCGAGTACAACTTTACG 445  
Dd 311 ATCCTTTGCTCTTCAAAACCTCATGACCTTGTCCCATTTCTTGAGGTGAGTTATACG 370  
Qy 446 CCAAGGAGATGTTCCCGATCTCTCGGCTGTAGCCAGTCCAAAGACGTTCCGAAACCT 505  
Dd 371 CTAATAGCCAAATTCGGATCTCGCAAAAGTATCTTCTCTATGATCTTTTCTACACACA 430  
Qy 506 TACCGTTCGTTTCCCTAAAGGAAACGATCGAGAAACCCGGTGTGAAGTCTGTTACTTGT 565  
Dd 431 TGCATTTAAGCATTTGGTGAAGCCACCAACAAA---GCTTGAACCCGTTATGTGT 487  
Qy 566 GCGGAAACCCGTTTGACACATTTCTCTGTGTGCTTACCAACCAACATCAAAATCCG 625  
Dd 488 GTAGAGTATCAAGATACGTTGTCTCGGCTGTCATTTAGAAACATTTTGCATCGCA 547  
Qy 626 AGTCAGTACGCCAGTCTTGTAGACCAAGCTTTTGTATCTGTTTCCGGGAGTGTATCG 685  
Dd 548 CCAAGATGGATCAAGCCACTTTTGTAGCTCATGTTTGTGCTTATTTGTAGAGGTTCT 607  
Qy 686 GGTTCGCGCCGTTTTCGGAACACATGTTGGGATCTTGGAGAGAGAGCTTGAAGACCAAG 745  
Dd 608 TATAAGACCTTATTCGGAACATGTTTGAAGCTATTTGAAGAGGAGCTTGAAGCAAGG 667  
Qy 746 AGAAGTCTTTTAAAGTACGAGGATCTCAAGACGACATCGAGACCACTTTGAAGA 805  
Dd 668 AGAATGTTCTTTTCAATGAAGTACGAAGATTAATTTGAGGAGCTCTGTTTCAAGTCAAG 727  
Qy 806 GGTTCGCAACTTTTGTAGAGCTTCTTTCACCGAAGAGAGAGAAACGAAAGGGAGTTTGA 865  
Dd 728 GACTCGCCAGTCTTGTGAATGCTCCATTCACCAAGGAGAGAGAAAGTGGATCGTGG 787  
Qy 866 AGCTATCCCGAGCTGTGTAGCTTCGAGATCTCAAGAGTTCGAGGTGAACAGTCAA 925  
Dd 788 AGGAGATCTTGAAGTGTGTAGTTCGAAATTTAAGCAATTTTGAAGGTTTAAAGAAATG 847  
Qy 926 ACAGTCTGATCAGAACTTTGAGAACTCGATCTTCTGTTTCGAAAGAGAGAGTGAAT 985  
Dd 848 GGACAAACGAGAAATGGTGTAGATTTCTCAGGTGTTCTTAGGAAAGGTGAGTTGTTGAT 907  
Qy 986 GGTTAACTATTGTTCACCTTCAAGTGAAGAAAGTGTACGCTTGTAGTGAATGCAAGT 1045  
Dd 908 GGAAGAAATCATCTTACGCCACAAATGCGCAAAACCTTTGATGAGATTTATGACTAGAC 967  
Qy 1046 TAGGTGATCTGTTCTCACTTT 1067  
Dd 968 TAGGAGACTCCGGTTTGATATT 989

## RESULT 6

US-09-938-842A-1027

; Sequence 1027, Application US/09938842A

Publication No. US20040009476A9  
GENERAL INFORMATION:  
APPLICANT: Harper, Jeff  
APPLICANT: Kreps, Joel  
APPLICANT: Wang, Xun  
APPLICANT: Zhu, Tong  
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
FILE REFERENCE: SCRIPI300-3  
CURRENT APPLICATION NUMBER: US/09/938,842A  
CURRENT FILING DATE: 2001-08-24  
PRIOR APPLICATION NUMBER: US 60/227,866  
PRIOR FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: US 60/264,647  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/300,111  
PRIOR FILING DATE: 2001-06-22  
NUMBER OF SEQ ID NOS: 5379  
SEQ ID NO 1027  
LENGTH: 996  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
US-09-938-842A-1027

Query Match 20.4%; Score 219.2; DB 11; Length 996;  
Best Local Similarity 53.0%; Pred. No. 5.1e-62;  
Matches 520; Conservative 0; Mismatches 453; Indels 9; Gaps 2;  
QY 86 AATCTCGCGAGCTCCCGAAGCGAAGGATGAAGGCTAAGCTGGAGTTCCCAAGAGA 145  
DB 17 AAGCTCATCCTTCCAAACTACATGAAGACGACAGCTTAGTCAAGAACCAAGAACT 76  
QY 146 TGTGGATCTCTCTTAAGGAGAGAGATCGAAGTCTGTACCTTTACCTATCCAAAG 205  
DB 77 TGATCACTTCTACCTTCAGACAAAGATTTCATGGGTATGCTCTCAACTACAAAG 136  
QY 206 GGTTTGGTGCAGCGCAAGCAAGATTCAGACCATCATCTTTCCAAAGCAATTCAT 265  
DB 137 GTTGTGGTATCTCAAAACATCTCAAGCGCTTGTAGCTCAAAACATCTCAAGC 196  
QY 266 CCCTCGAAACGAGCTGCTTCGCCACCAATACCTTAATCCGGTACCACTGGCTAAAG 325  
DB 197 CACGAGATACATGATATAATCTCGCTTTGCGCAAGGTTGAACCACTTGGCTCAAT 256  
QY 326 CTTTAACTTTTCAACATCTTAAACGTCACCGTTTGTATCGGTTGCTCGAGTACCAAC 385  
DB 257 CCCTAAATTTTCGCTGTGTATACATAGAGAAAGT-----ACCGCGGAACCCCTCAACAC 310  
QY 386 ACCCTCTTTTCACTTTCCAAACCTCATGACCTTGTACCTTTCTCGAGTACAAAGTTTACG 445  
DB 311 ATCCTTTGCTTTTACAAACCCCTCATGACCTTGTCCCATTTCTTGAGTTGAGTTATACG 370  
QY 446 CCAACGAGATGTTTCCCGATCTCTCGGCTGTCAGGCTTCAAGAACGTTCCGAACCCACT 505  
DB 371 CTAATAGCAAAATTCGGATCTCGCAAGATTTCTCTCTATGATCTTTTCTACACACA 430  
QY 506 TACGTTTCGGTTCCTTAAGAAACGATCGAGAACCCGGTGTGAAGTCTGTCTTGT 565  
DB 431 TGCATTTACAAGCATTGGTGAACCCACCAAAA---GCTTGAACACCCGTATATGTGT 487  
QY 566 GCCGGAACCCGTTTGAACATTCATCTCTTGTGGCATTTACCAACCAACATCAATPCCG 625  
DB 488 GTAGAGGTATCAAGATAGCTTTGCTCCGGCTGCAATATAGAAACATGTTGCATGCCA 547  
QY 626 AGTCAGTGGCCGCTTGTAGAACCATTTTGTATCTGTATTTGCTTATGCGGGGAGTATCG 685  
DB 548 CCAAGATGGATCAAGCACTTTTCAAGTCTCAATTTGATGCTTATTTAGAGGATTTCTCT 607  
QY 686 GGTTTGGCCGCTTTTGGAAACATATTTGGGATCTAGAGAGAGAGCTTGAAGAGACCA 745  
DB 608 TATATGACCTTATTTGGAACTGATTTAGCTATTTGGAAGGAGGAGCTTGGAGCAAGG 667  
QY 746 AGAAAGTCTCTTTTAAAGTACGAGGATCTCAAAAGACGACATCGAGACCAACTTGAAGA 805

DB 668 AGAATGTTCTTTTCATGAAGTACGAAGAGATTAATTGAGGAGCCCTCGTGTCAAGTCAAGA 727  
QY 806 GGCTTGCAACTTTCTTAGAGCTTCCCTTCCCGAAGAGAGGAAACGAAAGGGAGTTGTGA 865  
DB 728 GACTCGCCGAGTCTTTTGAATGCTCCATTCACCAAGGAAGAAAGAGTGGATCGGTGG 787  
QY 866 AGCTATCCGCGAGCTGTGTAGCTTCGAGAATCTGAAGAGTTGGAGGTGAACAAGTCAA 925  
DB 788 AGGAGATCTTGAAGTTGTGTAGTTTACGAAATTTAAGCAATTTTGGAGGTTAATAGAATG 847  
QY 926 ACAAGTCGATCAAGAACTTTGAGAATCGATTTCTTTTCGAAAGGAGAGTGAAGTGAAT 985  
DB 848 GGAACAAGAGAAATTTGGTGTAGATTTCTCAGTGTCTTTTAGGAAGGCTGAAGTTGGTGAAT 907  
QY 986 GGGTTAACTATTTGTCACTTCAAGTGGAAAGATTGTTCAGCTTTAGTGGATGACAAGT 1045  
DB 908 GGAAGAATCATCTTACGCCCAAAATGCGAAACCTTTGATGAGATTAATTGACTATAGAC 967  
QY 1046 TAGGTGGATCTGCTCTCACTTT 1067  
DB 968 TAGGAGACTCCGGTTTGATATT 989  
RESULT 7  
US-10-437-963-55857  
Sequence 55857, Application US/10437963  
Publication No. US20040123343A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
APPLICANT: Wu, Wei  
APPLICANT: Boukharov, Andrey A.  
APPLICANT: Barbazuk, Brad  
APPLICANT: Li, Ping  
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
FILE REFERENCE: 38-21(53221)B  
CURRENT APPLICATION NUMBER: US/10/437,963  
CURRENT FILING DATE: 2003-05-14  
NUMBER OF SEQ ID NOS: 204966  
SEQ ID NO 55857  
LENGTH: 1041  
TYPE: DNA  
ORGANISM: Oryza sativa  
FEATURE:  
OTHER INFORMATION: Clone ID: PAT\_MRT4530\_57824C.1  
US-10-437-963-55857  
Query Match 18.6%; Score 200.8; DB 17; Length 1041;  
Best Local Similarity 56.0%; Pred. No. 7.8e-56;  
Matches 448; Conservative 0; Mismatches 337; Indels 15; Gaps 3;  
QY 276 CGAGTCGCTTCTCGCCACCACCTAATATCCGGTACACCTGGCTAAAAGCTTTAACTTT 335  
DB 225 CGACATCATCTGTCGCCACCTTCCCAAGTCCGGCAGCAGTGGATCAAGGGCGCTCCTCTA 284  
QY 336 CACCATCTTTAAACCGTCAACCGTTTGTATCCGGTTTGCCTCGAGTACCAACCAACCTCTTTT 395  
DB 285 CGCCAGGTGTCACCG---GAGGAGACACCCCGCCGCGCCGCGCCGACCCCTTTTCA 341  
QY 396 CACTTCCAAACCTCATGACCTTGTACCTTTCTTCAGTACAGCTTTAGCCCAACGGAGA 455  
DB 342 CTCCTCGGCCCCCGAGTGCCTCAACTTCTCGAGTACCAAGCTCTACAGCTCTACCAACAACAG 401  
QY 456 TGTTCCTGATCTCTCGGGTCTAGCCAGTCCAAAGACGTTTCGCAACCCACTTACCTTCCG 515  
DB 402 AGTCCCGGACCTTGGCAGGCTCCCGAGCCCGAGGCTGTTCGCGACGACGCTCCCGTTTAC 461  
QY 516 TTCCCTTAAAGGAAACGATCGAGAAACCCCGGTGTGAAGTCTGTGTTACTTGTGCGCGAAACCC 575

Db 462 GTGCTGCCGAGCGCGCGCGCGCTCGGCTGCAAGTGTGTACGTGTGCGCGCACCC 521  
 Qy 576 GTTTGACACATTCTCTCTGTCGCAATACCAACAACATCAAAATCC---GAGTCAGT 632  
 Db 522 CAAGGACAACTGATCTCGATGTGGACTTCGCCCAACAAGTTCAAGGCGCGTGGAGGCA 581  
 Qy 633 GAGCCCACTCTGTAGACCAAGCTTTTGTATCTGATTTGCGGGAGTGATCGGTTTG 692  
 Db 582 GGAGCCCACTGTGCGCGGAGGCATCGCGAGCTGTCTGCTCGCGCTGCGCGTCCGG 641  
 Qy 693 CCCGTTTTGGGAACACATGTTGGGATCTGAGAGAGAGCTTTGAAGAGACCAAGT 752  
 Db 642 GCCGTACTGGACCACTCTCTGCTACTGCGCGCGCGCACTGCGCGCGCGCGAGCAGT 701  
 Qy 753 CTTCTTTTAAAGTACGAGGATCTCAAGAGACATCGAGACCACTTTGAAGAGCTTGC 812  
 Db 702 CTTCTTTTCAAGTACGAGGAGATGAAGCTCGACCGCGCGCGCACTGCGGAGGCTGGC 761  
 Qy 813 AACTTTCTTAGAGCTTCTTTTCCCGAAGAGAGCAACGAAGGAGTTGTGAAGGCTAT 872  
 Db 762 GGAGTTCTGTGCGCTCGCGCTTTCAGCGCGAGAGGAGAGTGGCGTGTGGAGCGCAT 821  
 Qy 873 CGCCGAGCTGTGATCTCGAATCTCGAAGTCTGAAGAGTGTGAGGTGAACAAAGTC 932  
 Db 822 CGTCAGGCTGTCTCGTTCGATCATGATCGGCTGAGGCGGACCAAGAGCGGCAAGAC 881  
 Qy 933 -----GATCAAGACTTTGAAATCGATCTTGTTCGAAAGGAGAGTGA 983  
 Db 882 GGAGCTGTGTGCGCGCGCGGCGGAATAGCTCATCTTCTCGTGTGCGGCGAGTCTGGGA 941  
 Qy 984 TTGGGTAACTATTTGTCACTTCAAGTGTGAAGATTTGACGCTTGTGAGTGAACA 1043  
 Db 942 CTGGCGGAACCATTTTCGCGGAGATTGCACAGCGATCGACCCATAACCGAGGCGAG 1001  
 Qy 1044 GTTAGGTGATCTGTCTCA 1063  
 Db 1002 GTTCAATGTTCCGCTCTCA 1021

## RESULT 8

US-10-195-144-87/c  
 ; Sequence 87, Application US/10195144  
 ; Publication No. US20030126646A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BROWN, GREGORY G.  
 ; APPLICANT: FORMANOVA, NATASA  
 ; APPLICANT: DENDY, CHARLES  
 ; APPLICANT: LANDRY, BENOIT S.  
 ; APPLICANT: CHEUNG, WING  
 ; APPLICANT: JIN, HUA  
 ; TITLE OF INVENTION: NUCLEAR FERTILITY RESTORER GENES AND METHODS OF USE IN  
 ; TITLE OF INVENTION: PLANTS  
 ; FILE REFERENCE: 16313-0136  
 ; CURRENT APPLICATION NUMBER: US/10/195,144  
 ; CURRENT FILING DATE: 2002-10-01  
 ; PRIOR APPLICATION NUMBER: 60/305,026  
 ; PRIOR FILING DATE: 2001-07-12  
 ; PRIOR APPLICATION NUMBER: 60/305,363  
 ; PRIOR FILING DATE: 2001-07-13  
 ; PRIOR APPLICATION NUMBER: 60/308,736  
 ; PRIOR FILING DATE: 2001-07-30  
 ; NUMBER OF SEQ ID NOS: 128  
 ; SOFTWARE: Patentin Ver. 2.1  
 ; SEQ ID NO 87  
 ; LENGTH: 271990  
 ; TYPE: DNA  
 ; ORGANISM: Raphanus sativum  
 ; FEATURE:  
 ; NAME/KEY: modified base  
 ; LOCATION: (144241)..(144300)  
 ; OTHER INFORMATION: a, t, c, g, other or unknown  
 US-10-195-144-87

Query Match 17.1%; Score 184.2; DB 15; Length 271990;  
 Best Local Similarity 53.5%; Pred. No. 9, 4e-49;  
 Matches 485; Conservative 0; Mismatches 403; Indels 19; Gaps 4;  
 Qy 114 AGATGAAGGGCTAAGTCGAGTTCGAAGAGATGTTGGATCTCTCTTAAGGAGAGG 173  
 Db 244850 AGACACAAAGTAAGTGAAGAAACAGGAAGGTGATCTCTTCGCTCTCCACACAGA 244791  
 Qy 174 ATGAGAACTCTCTTACCTTATCCAAAGGTTTGGTCCCAAGCAAGAGATTCA 233  
 Db 244790 TTACCAAGGCAATAGATTGTAATATCAAGATGTTGGTATATTACACACCTTCA 244731  
 Qy 234 AGCCATCATGTCTTTCCAAAAACATTTCCAAATCCCTCGAAAAACAGCTGTTCTCGCCAC 293  
 Db 244730 AGGTGTC-TCAATTTCCAGAGAGGTTTCAACCGCAAGACACTGATGTAATCATTTGCTTC 244672  
 Qy 294 CATACCTAAATCGGTACAACTGCTTAAGCTTTAACTTTTCAACATCCCTTAACCGTCA 353  
 Db 244671 GTACCCCAATCAGGCACTTACTTGGCTCAAGGCCCTCAAGTGGCTGTGTTGAGAGATC 244612  
 Qy 354 CGGTTTGTATCCGTTGCTTCCAGTACCAACCAACCTCTTTTCACTTCCAACTCATGA 413  
 Db 244611 AAGAACCACTCTTCTG-----ATCATCTCTCTTATATATAATCTCTCATGG 244564  
 Qy 414 CTTGTACTTCTTTCGAGTACAAGCTTTTACCCAAACGAGATGTTCCGATCT---CTC 470  
 Db 244563 CATATACCATCTTCTGGAGATCGATGTGTACCAGAAAGCTCAAGTCTCTAAGCTAGCCAA 244504  
 Qy 471 GGGTCTAGCCAGTCCAAAGAACCTTCGCAACCACTTACCGTTCCGTTCCCTAAAGGAAAC 530  
 Db 244503 GTTCTCAGCACTTCCGAGCTGTTCTCGACTCACATGCCACTGCACAGTCCACAGG 244444  
 Qy 531 GATCGAAGAACCCGGTGTGAAGTGTGTGTCGCGGAACCCGTTTGAACATTCAT 590  
 Db 244443 ACTCAAGCACTCTCTTGTCAAGATGTGTACGTGTGCAAGACGTGAAGGACACGTTGAT 244384  
 Qy 591 CTCTTCGTGCAATACACCAACAAATCAATCAATCCAGTCAAGTCCAGTCTTCTAGTA 650  
 Db 244383 CTGCTGTGGTTTTACGCTGTGCTATATAATAAATCGAACCAACAGAGATTTCTGA 244324  
 Qy 651 CCAAGCTTTTGTATCTGTATTGCGGGGAGTGTGCGGTTTGGCCGTTTGGGAAACAT 710  
 Db 244323 GTCTATGTTTAAAGAGTCTCTGCGATGGAACCACTATTATTGGACCTTTTGGGATCATCT 244264  
 Qy 711 GTTGGGATCTGAGAGAGAGCTTGAAGACACAGAAAGTCTTCTTTTAAAGTACGA 770  
 Db 244263 CTTGAGTTACTGAGAGAGAGCTTGAAGACCCCAAGCATGCTTTTCTGAGGATGA 244204  
 Qy 771 GGATCTCAAAGACGACATCGAGACCACTTGAAGAGGCTTGCACCTTTCTTAGAGCTTC 830  
 Db 244203 GGAGATGAAGCGGAGCTTCGTCGATCAGATCAAGAGACTTTCGGGATGTC 244144  
 Qy 831 TTTCAACGAAGAGAGAGAGAGAGGAGTGTGAAGGCTATCGCGAGCTGTGAGCTT 890  
 Db 244143 TTTTACTAAGCAAGAGAGAGATAGTGTGATCTGTGGCGGGATCTTGGACCTCTGCTCTCT 244084  
 Qy 891 CGAGATCTGAAGAGCTTGAAGTGAACAAGTCAACAAGTCAACAAGTCAACAAGTGA 950  
 Db 244083 GCGTAATCTGAGCAGTTTGAAGGCTTAACA---ACAGGCAATTAACAATGTTGAGCA 244027  
 Qy 951 TCGATCTTCTTTCGGAAAGGAGAGTGTGAGTGAAGTGGGTTAATCTTTCTCCTTCA 1010  
 Db 244026 CAAGTTTTTTTCCGTAAAGAGAGAGTGTGAGTGTGACTCGAAAAATTTCTTACGCTCTGAAT 243967  
 Qy 1011 AGTGGAA 1017  
 Db 243966 GGAGAAA 243960

## RESULT 9

US-10-345-072-87/c  
 ; Sequence 87, Application US/10345072  
 ; Publication No. US20030237112A1

```

; GENERAL INFORMATION:
; APPLICANT: BROWN, GREGORY G.
; APPLICANT: FORMANOVA, NATASA
; APPLICANT: DENDY, CHARLES
; APPLICANT: LANDRY, BENOIT S.
; APPLICANT: CHEUNG, WING
; APPLICANT: JIN, HUA
; APPLICANT: LAI, FANG MING
; APPLICANT: LEFOREST, MARTIN
; TITLE OF INVENTION: NUCLEAR FERTILITY RESTORER GENES AND METHODS OF USE IN
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 16313-0210
; CURRENT APPLICATION NUMBER: US/10/345,072
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/22217
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: 60/305,026
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/305,363
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/308,736
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 87
; LENGTH: 271990
; TYPE: DNA
; ORGANISM: Raphanus sativum
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (144241)..(144300)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-345-072-87

Query Match 17.1%; Score 184.2; DB 16; Length 271990;
Best Local Similarity 53.5%; Pred. No. 9, 4e-49;
Matches 485; Conservative 0; Mismatches 403; Indels 19; Gaps 4;

QY 114 AGATGAAGGCTTAAGCTGGAGTCCAGAGATGTGGATCTCTCTCTAAGGAGAGAGG 173
DB 244850 AGACGACAGATAAGTGAAGAACAGGAGGTATCTCTTCGTTCTTCCACACAGA 244791

QY 174 ATGGAGAACTCGTTACCTTACCTATCCAGGGTTTGGTCCCAAGCAAGATCA 233
DB 244790 TTACCAAGGCAATAGATTGTAAATATCAAGGATGTGGTATTATTAACAACCCCTCCA 244731

QY 234 AGCCATCATGCTTTCCAAAACATTTCCAACTCCCTCGAAAACGACGTCTCTCGCCAC 293
DB 244730 AGGTGTC-TCAATTTCCAGAGAGGTTTCAACCGCAAGACACTGATGTAAATCATGTCTC 244672

QY 294 CATACCTAAATCCGTACAACTGGCTAAAAGCTTTAACTTTCACTTCCACCTTAAACCGTCA 353
DB 244671 GTACCCCAATCAGGCACACTACTTGGCTCAAGGCCCTCACAGTCGCTCTGCTTGAGATC 244612

QY 354 CCGGTTTCATCCGGTTGCTCGAGTACCAACACCCCTCTTTTCACTTCCAAACCTCATGA 413
DB 244611 AAAGAACCACTCTCTG-----ATCATCTCTCTATATCATATCTCTCATGG 244564

QY 414 CTTGTACTCTTTCAGAGTACAGCTTTTACGCAACGAGATGTTCCCGATCT---CTC 470
DB 244563 CATTATACCAATCTTGGAGATCGATGTGTACCAAGAGCTCAAGTCTCAACCTAGCCAA 244504

QY 471 GGGTCTAGCCAGTCCAAAGAGCTTGGCAACCCACTTACCGTTCCGTTCCCTTAAGGAAC 530
DB 244503 GTTCTCAGCACTCCGAGGCTGTCTCGACTCATGCTCAATGCCACTGCACAGATCCACGAGC 244444

QY 531 GATCGAGAAACCCGGTGTGAAGGTCGTGTACTTGTGCGGGAACCCGTTTGAACACATTCAT 590
DB 244443 ACTCAAGCACTCTCTCTTCAAGATTGTGTACGTGTGAGGAAGCTGAAGGACACAGTTGAT 244384

QY 591 CTCCTCGGGCATTTACACCAACACATCAATCCGAGTCAGTGAAGCCAGCTTCTGTGAGA 650
DB 244383 CTCGTGTGGTTTACAGCTGTGTCTATATATAAATAACCAACCAAGAGAGTCTCGA 244324
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## RESULT 10

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US-10-195-144-80
; Sequence 80, Application US/10195144
; GENERAL INFORMATION:
; APPLICANT: BROWN, GREGORY G.
; APPLICANT: FORMANOVA, NATASA
; APPLICANT: DENDY, CHARLES
; APPLICANT: LANDRY, BENOIT S.
; APPLICANT: CHEUNG, WING
; APPLICANT: JIN, HUA
; TITLE OF INVENTION: NUCLEAR FERTILITY RESTORER GENES AND METHODS OF USE IN
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 16313-0136
; CURRENT APPLICATION NUMBER: US/10/195,144
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/305,026
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/305,363
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/308,736
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 2067
; TYPE: DNA
; ORGANISM: Raphanus sativum
US-10-195-144-80
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Query Match 15.4%; Score 166; DB 15; Length 2067;
Best Local Similarity 53.7%; Pred. No. 5, 6e-44;
Matches 421; Conservative 0; Mismatches 345; Indels 18; Gaps 3;

QY 237 CATCATGTCTTTCCAAAAACATTTCCATCCCTCGAAAACGACGCTGTTCTCGCCACCCT 296
DB 282 CATTTTCCGGTTTGGAGAGTTTCAACCGCAAGACACTGATGTAATCATTTCTTCGTA 341

QY 297 ACCTAATCCGTACACCTGCTAAAGCTTTAACTTTCACATCTTAAACGTCACCG 356
DB 342 CCCCAATCAGGCACTACTTGGCTCAAGGCCCTCAAGTCGCTCTGCTTTGAGAGATCAA 401

QY 357 GTTTGATCCGGTTGCTCGAGTACCAACCAACCTCTTTTCACTTCCAAACCTCATGACT 416
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Db 402 GAACACATC-----TTCTGATCATCTCTCTCTATATCATATCTCATGCGAT 449  
Qy 417 TGTACCTTTCTTCGAGTACAAGCTTTAGCCAAAGGAGATGTTCCCGATCT---CTCGGG 473  
Db 450 TATACCAATCTTGGAGATCGATGTGTACACGAAAGCTCAAGTCTTAACCTAGCCAAAT 509  
Qy 474 TCTAGCCAGTCCAGAAAGCTTGGCAACCACTTACCGTTGCGTTCCCTAAAGGAAACGAT 533  
Db 510 CTCAGCACTCCGAGCTGTTCTCGACTCAATGCCACTGACAGATCCAGAGCACT 569  
Qy 534 CGAGAAACCCGGTGTGAAGGTGTTACTTGTGCGGAAACCGTTTGACACATTCATCTC 593  
Db 570 CAAAGCACCTCTCTTCCAAAGATTGTGTAGCTGTGAGGAAACGTGAAGGACACGTTGATCTC 629  
Qy 594 TTCGTGGCATTACACCAACCAATCAATCCGAGTCACTGAGCCAGCTTGTCTAGACCA 653  
Db 630 GTGTTGGTTTACAGCTGTGCTATATAAAATCGAACCAACCAAGAGATCTCGAGTC 689  
Qy 654 AGCTTTTGATCTGATTTGCGGGGAGTGTATCGGGTTTGGCCCGTTTGGGAAACATGTT 713  
Db 690 TATGTTTACGAGTCTCGGATGGAACCACTATTTTGGACCTTTTGGGATCATCTCT 749  
Qy 714 GCGATCTGGAGAGAGCTTGAAGAGCCAGAGAAAGTCTTCTTTTAAAGGTACGAGGA 773  
Db 750 GAGTTTACTCGAGAGAAAGCTTGGAAAGCCCAAGCATGTCTCTTTTCATGAGGTATGAGGA 809  
Qy 774 TCTAAGACGACATCGAGAACCACTTGAAGAGCTTGCACCTTTCTTAGAGCTTCTCTT 833  
Db 810 GATGAAGCCGAGCTCTGTGATCAGATCAAGAGATTTGGGACTTCTTGGGATGCTCTT 869  
Qy 834 CACCGAAGAGAGGAAACGAAAGGGAGTTGTGAAGGCTATCGCCGAGCTGTGTAGCTTGA 893  
Db 870 TACTAAGCAAGAAAGATAGTGGATCTGTGACGGGATCTTGACCTCTCTCTCTGCG 929  
Qy 894 GAATCTGAAGAGTTGGAGGTGAACAGTCAACCAAGTCGATCAAGAACTTTGAGATCG 953  
Db 930 TAATCTGACAGCTTTGGAGGCTTAACAA---AACAGGACAAATAACATGTGGAGCAAA 986  
Qy 954 ATCTTGTGTTCCGAAAGGAGAGTGAAGTGAATGGGTTAACTATTTGTCACCTTCACAAGT 1013  
Db 987 GTTCTTTTCCGTAAAGGAGAGTGGTGACTCGAAATAATATCTTACGTCTGAAATGGA 1046  
Qy 1014 GGAA 1017  
Db 1047 GAAA 1050

## RESULT 11

US-10-345-072-80  
; Sequence 80, Application US/10345072  
; Publication No. US20030237112A1  
; GENERAL INFORMATION:  
; APPLICANT: BROWN, GREGORY G.  
; APPLICANT: FORMANOVA, NATASA  
; APPLICANT: DENDY, CHARLES  
; APPLICANT: LANDRI, BENOIT S.  
; APPLICANT: CHEUNG, WING  
; APPLICANT: JIN, HUA  
; APPLICANT: LAI, FANG MING  
; APPLICANT: LEFOREST, MARTIN  
; TITLE OF INVENTION: NUCLEAR FERTILITY RESTORER GENES AND METHODS OF USE IN  
; FILE OF INVENTION: PLANTS  
; FILE REFERENCE: 16313-0210  
; CURRENT APPLICATION NUMBER: US/10/345,072  
; CURRENT FILING DATE: 2003-01-16  
; PRIOR APPLICATION NUMBER: PCT/US02/22217  
; PRIOR FILING DATE: 2002-07-12  
; PRIOR APPLICATION NUMBER: 60/305,026  
; PRIOR FILING DATE: 2001-07-12  
; PRIOR APPLICATION NUMBER: 60/305,363  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: 60/308,736

; PRIOR FILING DATE: 2001-07-30  
; NUMBER OF SEQ ID NOS: 179  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 80  
; LENGTH: 2067  
; TYPE: DNA  
; ORGANISM: Raphanus sativum  
; US-10-345-072-80

Query Match 15.4%; Score 166; DB 16; Length 2067;  
Best Local Similarity 53.7%; Pred. No. 5.6e-44;  
Matches 421; Conservative 0; Mismatches 345; Indels 18; Gaps 3;  
Qy 237 CATCATGCTTTTCCAAAAACATTTCCATCCCTCGAAAAAGACGTCGTTCTCGCCACCAT 296  
Db 282 CATTTTCCGGTTTTCAGAGAGTTTTCACCCGAAGACACTGATGATTAATCATTGCTTCGTA 341  
Qy 297 ACCTAAATCCGTTACAACTGCTTAAAGCTTTAACTTTCAACCATCTTTAAACCGTCACCG 356  
Db 342 CCCCAATCAGGACATCTTGGCTCAGGCCCTCAGTCGCTCTGCTTGAGAGATCAAA 401  
Qy 357 GTTTGATCCGGTTGCTCGAGTACCAACCACTCTTTTCACTTCCAAACCTCATGACT 416  
Db 402 GAACCACTC-----TTCTGATCATCTCTCTATATCATATAATCTCATGGCAT 449  
Qy 417 TGTACCTTTCTTCGAGTACAAGCTTTTACGCCAACCGGAGATGTTCCCGATCT---CTCGGG 473  
Db 450 TATACCAATTTTGGAGATCGATGTGTACCAAGAAAGCTCAAGTCTTACCTAGCCAAAT 509  
Qy 474 TCTAGCCAGTCCAAAGAAACGTTGCGCAACCACTTACCGTTTCGGTTCCCTAAAGAAACGAT 533  
Db 510 CTGAGACCTCCGAGCTGTTCTCGACTCAGATGCCATGACACGATCCAGAAAGCACT 569  
Qy 534 CGAGAAACCCGGTGTGAAGGTGTGTACTGTGTGCGGAAACCGTTTGACACATTCATCTC 593  
Db 570 CAAAGCACTCTCTTTCGAAGATTGTGTACGTGTGCAAGAAACGTGAAGGACACGTTGATCTC 629  
Qy 594 TTCGTGSCATTACCAACCAACATCAATCCGAGTCAGTGAGCCCACTTCTCTAGACCA 653  
Db 630 GTGTTGGTTTACAGCTGTGCTATATAAAATCGAACCAACCAAGAGAGTTTCTCGAGTC 689  
Qy 654 AGCTTTTGATCTGTATTTGCGGGGAGTGTATCGGGTTTGGCCCGTTTGGGAAACATGTT 713  
Db 690 TATGTTTAAAGAGTCTTCTGCGATGGAACCACTATTTTGGACCTTTTGGGATCATCTCT 749  
Qy 714 GGGATCTCGAGAGAGCTTTGAAGAGACACAGAAAGTCTTCTTTTAAAGGTACGAGGA 773  
Db 750 GAGTTACTGGAGAGAGCTTGGAAAGCCCAAGCATGTCTCTTTTCATGAGGTATGAGGA 809  
Qy 774 TCTCAAAGACGACATCGAGACCAACTTGAAGAGGCTTGCACCTTTCTTGAAGCTTCTCTT 833  
Db 810 GATGAAGCCGAGCTCTGCTGATCAGATCAAGAGACTTGGGAGCTTCTTGGGATGCTCTT 869  
Qy 834 CACCGAAGAGAGGAAACGAAAGGGAGTGTGTGAAGGCTATCGCCGAGCTGTGTAGCTTGA 893  
Db 870 TACTAAGCAAGAAAGATAGTGGATCTGTGACGGGATCTTGACCTCTCTCTCTGCG 929  
Qy 894 GAATCTGAAGAGTTGGAGGTGAACAGTCAACCAAGTCGATCAAGAACTTTGAGATCG 953  
Db 930 TAATCTGACAGCTTTGGAGGCTTAACAA---AACAGGACAAATAACATGTGGAGCAAA 986  
Qy 954 ATCTTGTGTTCCGAAAGGAGAGTGAAGTGAATGGGTTAACTATTTGTCACCTTCACAAGT 1013  
Db 987 GTTCTTTTCCGTAAAGGAGAGTGGTGACTCGAAATAATATCTTACGTCTGAAATGGA 1046  
Qy 1014 GGAA 1017  
Db 1047 GAAA 1050

## RESULT 12

US-10-437-963-55524  
; Sequence 55524, Application US/10437963



Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 5524  
; LENGTH: 1077  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_57523C.1  
US-10-437-963-5524

Query Match 15.0%; Score 161.8; DB 17; Length 1077;  
Best Local Similarity 51.1%; Pred. No. 9.5e-43;  
Matches 444; Conservative 0; Mismatches 407; Indels 18; Gaps 2;

QY 205 GGGTTTGGTCCGAGCAAGAGATTCAAGCCATCACTGTTTCCAAAACATTTCCAA 264  
Db 175 GGATTCTGTACCGCGCACCTGATCGCGCGACGCTGGCGCGGACACATTCGTG 234  
QY 265 TCCCTCGAAAAACGAGCTGTTCTGCCACCATCACTAAATCCGGTACAACTGGCTAAAA 324  
Db 235 GCCGCGCCCGAGCTATCTGCCACCATGCCAAGTCCGAGTCCGCTCAAG 294  
QY 325 GCTTTAACTTTCAACATCTTAACCGTCAACCGTTTGAATCGGTTGCTCGAGTACCAAC 384  
Db 295 CGCTCGCTTCTGCTGTCAGCGCGCGCGCACCGCGCGCGCGCGCGCGCACCG 354  
QY 385 CACCTCTTTTCACTTCCAACTTCATGACCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 444  
Db 355 CTCCTCCACTCCAGCGCGCAGCTGTCGTCATCTCTGCACTCTTCTGCACTCTTCTGAGATCAGC 414  
QY 445 GCCAACGAGATGT-----TCCGATCTCTCGGCTAGCAGTCCAGTCCAAAGAACGTTTC 495  
Db 415 CGCAGTCCGCGTCCG 474  
QY 496 GCACCCACTTACCGTTGCTTCCCTAAGAAACGATCGAAGAACCGCGGTGTGAAGTTC 555  
Db 475 GCAGTGCACGAACCGCTCTCGAGCGCTGCCCGCTCGGTCAAGCGCTCCGGGTGCCGCGTC 534  
QY 556 GTGTACTTGTCCGGAACCGCTTTTGACACATTCATCTCTTCTGTCGCAATTACCAACAAAC 615  
Db 535 GTCTACCTGTCCGCGGACCCCAAGACGCTTCTGCTCGCTCCGCGCAATTACCTCGACGAG 594  
QY 616 ATCAAAATCCGAGTCAGTAGCCAGTCTTGTAGACCAAGCTTTTGTATCTGTATTCGCGG 675  
Db 595 ATCAAAACAGAGGATCCACCATGACGCGCTTCGACGAGGCTTCGAGCTGCTCTGGAC 654  
QY 676 GGAGTGTGCGGTTTGGCGCGCTTTGGGAACACATGTTGGATCTCGAGAGAGAGCTTG 735  
Db 655 GCGTCTCGCGTACGGGCTTATGTGGGACCAACCGCGCGGAGTACTGGAAGGAGAGCTG 714  
QY 736 AAGAGACAGAGAAAGTCTTCTTTTAAAGGTACGAGGATCTCAAAGACGACATCGAGACC 795  
Db 715 GCGCGCGCGAGGAGGTGCTGCTTCTCGGTACGAGAGCTCAAGGAGGAGCGGCTGGGG 774  
QY 796 AACTTGAAGAGCTTGCACTTCTTAGAGCTTCTTTCACCGAAGAGAGAGAGAGAG 855  
Db 775 ACGGTGAGGCGCTCGCGCGCTTCTCGGCTGCGCGCTTACCGCGGAGAGAGCTTTCGCGGT 834  
QY 856 GGAGTTGTGAAGGCTATCGCGGAGTGTGTAGCTTCGAGATCTGAAGAAAGTTGGAGGTG 915

Db 835 GCGTCCCCGAAACTATCTGTGAGCTCTGCAGTATGAAAAGGATGAGAAACGTGGAGCA 894  
QY 916 AA-----CAAGTCAAAACAAAGTCGATCAAGAACTTTGAGAATCGATTCTTTGTTTCGG 966  
Db 895 AATCGAGACGGGAGCACGGGGCTACCTGTCGTCTCAAGAACTCGGCGCTTCTTCAGG 954  
QY 967 AAGGAGAAAGTGAAGTGAATTTGGTTAACTATTTGTACCTTCAAGTGAAGAAAGTTGTCA 1026  
Db 955 AAGGGTGAAGTGGAGACTGGAAGGAGCACATGTGCGCGGAGATGCGCGGAGGCTCGAC 1014  
QY 1027 GCCTTAACTGATGACAAAGTTAGTGTGATC 1055  
Db 1015 GACGTCGTGGAGGAGGCTGCGAGGCTC 1043

RESULT 13  
US-10-021-323-11330  
; Sequence 11330, Application US/10021323  
; Publication No. US20040123340A1  
; GENERAL INFORMATION:  
; APPLICANT: Deikman, Jill  
; APPLICANT: Feng, Paul C.C.  
; APPLICANT: Fincher, Karen L.  
; APPLICANT: Ziegler, Todd E.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(52274)B  
; CURRENT APPLICATION NUMBER: US/10/021,323  
; CURRENT FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: US 60/255, 619  
; NUMBER OF SEQ ID NOS: 17880  
; SEQ ID NO 11330  
; LENGTH: 654  
; TYPE: DNA  
; ORGANISM: Gossypium hirsutum  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(654)  
; OTHER INFORMATION: unsure at all n locations  
; OTHER INFORMATION: Clone ID: LIB3829-001-Q1-K6-G6  
US-10-021-323-11330

Query Match 14.6%; Score 157; DB 17; Length 654;  
Best Local Similarity 56.9%; Pred. No. 2.8e-41;  
Matches 355; Conservative 0; Mismatches 251; Indels 18; Gaps 3;

QY 294 CATACCTAAATCGGTACAACTGGCTAAAGCTTTAACTTTACATCTTCAAGTCTTAAACGTC 353  
Db 1 CTTTTCCTCAATGTGGTACTTCTGGCTCAAGGCTTGAATTTCTCCACTTTTGTACCGCAA 60  
QY 354 CGGTTTGTATCGGTTGCTCGAGTACCAACCACTCTTTTCACTTCCAACTTCAATCA 413  
Db 61 TCAGTTCCATCGGATG-----AAATTCATGCTCCTTTTGGCGCTTCACTCA 108  
QY 414 CTTGTACCTTTCTTTCGAGTACAAGCTTTACGCCAAACGAGATGTTCCGATCTCTCGGG 473  
Db 109 ACTTGTTCGTTCTTTCGAGTATGATCTTTACTTTGAACCACTTTTCTCTGATCTTCGAAA 168  
QY 474 TCTAGCCAGT-----CCAGAACGTCGCAACCACTTACCGTTCCGTTCCCTAAGGA 528  
Db 169 GTTGTGCTTATCAGCAAGGCTTTTTCACCCAGGCTTTATGCTACTTTTGCAACT 228  
QY 529 AGCATCGAAGAACCGGCTGTGAAGTGTGATGTTGTGCGGAAACCGCTTTGACACATTC 588  
Db 229 TCCATTAAAGGATCTGCGCTGTAAGATGTTTACATATGTAGAAACCCCATGATATCTTC 288  
QY 589 ATCTCTTCGCTGAGATTACCAACCAACATCAAAATCGAGTCAAGTCAAGTCAAGTCAAGT 648  
Db 289 ATTTCTCTTTGGCTTTTCTCTGCAAGCTTCGAGACAAAAACCAAGAGTCACTATCACTA 348  
QY 649 GACCAAGCTTTTGTATCTGTATTGCGGGGAGTGTGGGCTTTTGGCGGCTTTTGGGAAAC 708





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Qy 237 CATCATGTCCTTTTCAAAAACATTTCCRAATCCCTCGAAAAACGAGTCGTCTCTCGCCACCAT 296
| | | | |
Db 177 GGTATGTTGGCGGCGCGCCACTTTCACCGCCCGGACACCGACATCATATCGCCACCTT 236
| | | | |
Qy 297 ACCTAATCCCGGTACAACCTCGCTAAAGCTTTAACTTTACCAATCCCTTAAACCGTACCG 356
| | | | |
Db 237 CCCCAGGTGTGGCACCACTGGCTCAAGGCGCTCTCTTCGCGACCGTCCACCGCGACGG 296
| | | | |
Qy 357 -GTTTGTATCCGGTTGCTTCGAGTACCAACACCTCTTTTCACTTC-----AACCC 407
| | | | |
Db 297 CGGCGCGCCCGCGGCTTGGAGGACGACGCGCGCGCTCGCGAGCTCAGGGCGGGAACCC 356
| | | | |
Qy 408 TCATGACCTTTAGCTTTCTTCGAGTACAAGCTTTAGCCCAACCGAGATGTTCCCGATCT 467
| | | | |
Db 357 GCACAGCTCTCCCGCTTCTCGAGATCCAGGTGTACGTGCGGACAGGGCGCGCGACCT 416
| | | | |
Qy 468 CTCGGTCTAGCCAGTCCAGAACGTTCCGAACCCACTTACCCTTCGGTTCCTTAAAGGA 527
| | | | |
Db 417 GAGTCCCTCCCGCGCCACCGCTCTTCGGACGACATCCCGCGCCCTCCCTGCGCGC 476
| | | | |
Qy 528 AACGATCGAGAAACCGGTTGAAAGTCTGTACTTGTGCGGAAACCGCTTTGACACATT 587
| | | | |
Db 477 CTCGTGCGCATCTCCGGCTCAAGGTGGTGTACATGTGCGCGACCCCAAGGACTGCCT 536
| | | | |
Qy 588 CATCTCTTGGGCAATTACACCAACAATCAAAATCCGAGTCACTAGTGAAGCCGCTTTGCT 647
| | | | |
Db 537 CGTCTCGCTGTGGCACTTCTTGGACCGCGCGGCGAGCCACGCGCGGACGCTC----- 591
| | | | |
Qy 648 AGACCAAGCTTTTTCATCTGTATTCCCGGGAGTGTATCGGTTTGGCCCGCTTTGGGAACA 707
| | | | |
Db 592 -GGCGAGACTTCCGCTCTTCTCGACGGCGTCTCGCTGGTCCGGCCGCTACTGGGACCA 650
| | | | |
Qy 708 CATCTTGGGATCTGGAGAGAGACTTTGAAGAGACCAAGAGAAAGTCTTCTTTTAAAGTA 767
| | | | |
Db 651 CGTCTGGCTTACTGGCGTGGCACGTTCGAGCGGCGCGGCGAGGTGCTGTTTCATGACGTA 710
| | | | |
Qy 768 CGAGGATCTCAAGACGACATCGAGACCACTTGAAGAGGCTTGCACACTTCTTAGAGCT 827
| | | | |
Db 711 CGAGGAGCTGAGCGGCGACAGCTGCGGCGAGCTGCGCCCTCGCGAGTTCGTCGGCCG 770
| | | | |
Qy 828 TCCCTTCACCGAGAGAGAGAAACGAAAGGGAGTTGTGAAGGCTATCGCCGAGCTGTGTAG 887
| | | | |
Db 771 GCCGTTCAACCGCGAGAGCGGGCGGCGCGGCTGGACGAGCGGATCGTGAAGGCGTGACG 830
| | | | |
Qy 888 CTTGAGAACTGAAGAGTTGGAGGTGAACAAGTCA 924
| | | | |
Db 831 CTTGAGAGCCTAGCGGCGCGGAGGTGAACAGGTCA 867
| | | | |
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Job time : 1842 secs

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